

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2003, 09:15:23 ; Search time 1230 Seconds
(without alignments)
698.457 Million cell updates/sec

Title: US-10-033-243-132

Perfect score: 21

Sequence: 1 tcgtcgaactcgcagatgat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2688711 seqs, 2045481386 residues

Word size : 0

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
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41: em_hcgo_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	6	AX592442
2	19	90.5	19	6	AX592329
3	19	90.5	22	6	AX592340
4	16	76.2	18	6	AX592324
5	16	76.2	119972	2	AP004029
6	16	76.2	126038	2	AP000367
7	16	76.2	144952	2	AP005629
8	16	76.2	146568	2	AC141727
9	16	76.2	166304	2	AC130730
10	15	71.4	22	6	AR287741
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12	15	71.4	22	6	AR287743
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15	15	71.4	22	6	AX046993
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18	15	71.4	22	6	AX135650
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99 14 66.7 103234 2 AP003997
100 14 66.7 113025 2 AC109596

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ALIGNMENTS

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RESULT 1
LOCUS AX592442 21 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 132 from Patent WO02052002.
ACCESSION AX592442
VERSION AX592442.1 GI:27950544
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 132 04-JUL-2002;
DynaVax Technologies Corporation (US)
LOCATION/Qualifiers
FEATURES
source
1..21
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 5 a 4 c 6 g 6 t
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Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTGAACGTTGAGATGAT 21
DB 1 TCGTGAACGTTGAGATGAT 21

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RESULT 2
LOCUS AX592329 19 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 19 from Patent WO02052002.
ACCESSION AX592329
VERSION AX592329.1 GI:27950431
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 19 04-JUL-2002;
DynaVax Technologies Corporation (US)
LOCATION/Qualifiers
FEATURES
source
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/note="Polynucleotide containing CG"
BASE COUNT 4 a 4 c 6 g 5 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTGAACGTTGAGATG 19
DB 1 TCGTGAACGTTGAGATG 19

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RESULT 3
LOCUS AX592340 22 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 30 from Patent WO02052002.
ACCESSION AX592340
VERSION AX592340.1 GI:27950442
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 30 04-JUL-2002;
DynaVax Technologies Corporation (US)
LOCATION/Qualifiers
FEATURES
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 5 a 4 c 7 g 6 t
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Query Match 90.5%; Score 19; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTGAACGTTGAGATG 19
DB 4 TCGTGAACGTTGAGATG 22

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RESULT 4
LOCUS AX592324 18 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 14 from Patent WO02052002.
ACCESSION AX592324
VERSION AX592324.1 GI:27950426
KEYWORDS

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SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 Fearon, K.L. and Dina, D.
AUTHORS Immunomodulatory polynucleotides and methods of using the same
TITLE Patent: WO 02052002-A 14 04-JUL-2002;
JOURNAL Dynavax Technologies Corporation (US)
FEATURES location/Qualifiers
SOURCE 1..18
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 4 a 4 c 5 g 5 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 TCGAACGTTCCGAGATG 19
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Db 3 TCGAACGTTCCGAGATG 18

RESULT 5
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LOCUS Oryza sativa (japonica cultivar-group) chromosome 2 clone
DEFINITION OJ1136 D07, *** SEQUENCING IN PROGRESS ***.
AP004029
ACCESSION AP004029.1 GI:15130691
VERSION HTG_PHASE2.
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa nipponbare (GAS) genomic DNA, chromosome 2, BAC
cloned OJ1136 D07
JOURNAL Published Only in Database (2001)
REFERENCE 2 (bases 1 to 119972)
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Direct Submission
JOURNAL Submitted (08-AUG-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@lab.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
COMMENT The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
location/Qualifiers
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/mol_type="genomic DNA"
/cultivar="Nipponbare"
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/clone="OJ1136 D07"

BASE COUNT 34735 a 25005 c 25414 g 34818 t

ORIGIN

Query Match 76.2%; Score 16; DB 2; Length 119972;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CGAACGTTCCGAGATGA 20
|||||
Db 38384 CGAACGTTCCGAGATGA 38399

RESULT 6
AP000367 126038 bp DNA linear PLN 21-MAR-2002
LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,
DEFINITION clone: P0437H03 (contig b).
AP000367
ACCESSION AP000367.1 GI:5441876
VERSION AP000367
KEYWORDS Oryza sativa (japonica cultivar-group)
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Oryza sativa Nipponbare (GAS) genomic DNA, chromosome 2, PAC
clone: P0437H03 (contig b)
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 126038)
AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.
TITLE Direct Submission
JOURNAL Submitted (06-JUL-1999) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@lab.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/,
Tel: 81-298-38-7441, Fax: 81-298-38-7468)
COMMENT This PAC clone has 10 kbp sequence gap, which result in 2 contigs
(contig a, b). This sequence shows contig b. The orientation of the
sequence is from S86 to T7 of the PAC clone. Genes were predicted
from the integrated results of the following: GENSCAN1.0, BLASTN1.4,
BLASTX2.0 as well as SplicePredictor (October1998 version). The
genomic sequence was searched against the non-redundant database
NR (PIR, SWISSPROT, GENEPEPT, PDB) from MAF DMBank and the cDNA
sequence databases at RGP. Protein similarities of the coding
regions were searched against NRP with BLASTP2.0. ESTs represent
the identified cDNA sequences using BLASTN1.4 with the
corresponding DDBJ accession no. and RGP clone ID.
location/Qualifiers
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/mol_type="genomic DNA"
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/chromosome="2"
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2.4.1.186). (297341)"
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CVYIPITILINSGTPRSFHLTFEMLFEWMSLHRKATLIGLEGRANENWVTE
KLGNAIKRKSSSKSASAKSPRWDRNLNVTLSGAAPLPSGCGWDLAKGKHFIYLP
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13319..13331)
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CDS

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CTGHAVALLLVLRGSSLSBSLAPARTKVCSDSECDDDDDSDGSDSN"
complement(16578..17255)
/note="ESTs AU070372 (S13446), AU075541 (S0353) correspond to
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Similar to Arabidopsis thaliana BAC genomic sequence.
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19855..20113,20190..20488,21053..21389,21495..21645,
22169..22484,22743..22774,23219..24224))
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KEALFHTWSEIYGFISGYTTSAGVFPYDPSKLVKKGRQTRIRINDNSE
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VPLRCAPSPQAAAGVHMVYLVTWGDTVSALAFRVAQEVLDANLTLESSIY
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VAFPCISGCKLKCHESDPTLFTTIDPNITVEFQISQEBDEDDDEDFPTTKA
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VPASADPNVSRARRKARGARADERSPFF"
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OSRGEGILGVTGNAAPKRYATSOIABEELRLREVLPTSGTKAKPKITPKNEPR
HSAPOSMDGTDSVBERGPADEYALRKVYLLDENDELDKQLSQAEBSAVLEDEK
PALDOLVYVEGLVDPSQMOPRRL"
join(58631..58875,59008..59067,59212..59356,59467..59628)
/note="Similar to Arabidopsis thaliana BAC genomic
sequence. (AC002332)"
/codon_start=1
/protein_id="BAA82385.1"
/db_xref="GI:5441887"
/translaction="MAAAMATTAABEAVVALDKETLMGCGDAPPAAPCAEMET
FKEVNRTPKRRNVGLRLKALKAIDPQALALAAARKMEALDEBSGEPDOWID
CIKNVQESFPFGVCGSGLVVYIEBCVAFWHDDRYKIDRLYLKLEBYAAGCSEVI
FRPLEANOIGSHNTYLSYASVMSKRLKKAIEIFNLGIAR"
join(66733..66759,67025..67378)
/note="hypothetical protein"
/codon_start=1
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/db_xref="GI:5441888"

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Query Match 76.2%; Score 16; DB 8; Length 126038;
Best Local Similarity 100.0%; Pred. NO. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

5 CGAAGCTTCGAGATGA 20

Db 27299 CGAAGCTTCGAGATCA 27284

RESULT 7
AP005629

LOCUS

DEFINITION AP005629 144952 bp DNA linear HTG 08-AUG-2002
OSJNBa0004A19, *** SEQUENCING IN PROGRESS ***.

ACCESSION AP005629

VERSION AP005629.1 GI:22138853

KEYWORDS HTG; HTGS PHASE2.

SOURCE Oryza sativa (japonica cultivar-group)

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzaceae; Oryza.

REFERENCE 1
Sasaki, T., Matsumoto, T. and Katayose, Y.
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
clone: OSJNBa0004A19
Published Only in Database (2002)

JOURNAL 2 (bases 1 to 144952)

REFERENCE 2
Sasaki, T., Matsumoto, T. and Katayose, Y.
Direct Submission
Submitted (07-AUG-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail: tsasaki@nias.affrc.go.jp, URL: http://rsgp.dna.affrc.go.jp/
Tel: 81-298-38-7441, Fax: 81-298-38-7468)

COMMENT NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

FEATURES
source
1..144952
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="2"
/clone="OSJNBa0004A19"

BASE COUNT 41769 a 30336 c 30932 g 41813 t 102 others

ORIGIN

Query Match 76.2%; Score 16; DB 2; Length 144952;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGATCA 20
|||||
Db 33857 CGAAGCTTCGAGATCA 33872

RESULT 8
AC141727/c

LOCUS AC141727 146568 bp DNA linear HTG 19-MAR-2003

DEFINITION Apis mellifera clone CH224-57G3, WORKING DRAFT SEQUENCE, 25
unordered pieces.

ACCESSION AC141727

VERSION AC141727.1 GI:29123911

KEYWORDS HTG; HTGS PHASE1; HTGS_DRAFT.

SOURCE Apis mellifera (honeybee)

ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.

REFERENCE 1 (bases 1 to 146568)

AUTHORS Mziny, D.M., Adams, C., Adio-Oduola, B., Ali-Usman, F.R., Allen, C.,
Alshrooke, S.L., Ameratunga, H.C., Are, J.R., Ayale, M., Banks, T.,
Barbata, J., Benton, J., Bimaga, K., Blankenburg, K., Bonnin, D.,
Bouck, J., Bowls, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P.,
Buhay, C., Burck, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D.,
Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C.,
Cleveland, C.D., Cox, C., Coyle, M.D., Daborn, S.R., David, R.,
Davis, M.L., Davis, C., Davy-Carroll, L., Dedertich, D.A.,
Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H.,
Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J.,
Eamhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escoto, M.,
Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Franz, P.,
Gabris, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R.,
Gorrell, D.H., Guevara, M., Gunaratne, P., Hale, S., Hamilton, K.,
Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J.,
Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B.,
Homes, F., Howard, S., Huber, J., Hulvik, S., Hume, J., Jackson, L.E.,
Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S.,
Karlsom, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C.,
Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L.,
Li, J., Li, Z., Licharge, O., Lieu, C., Liu, J., Liu, W., Louised, H.,
Lozado, R.J., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J.,
Maheshwari, M., Mapa, P., Martin, R., Martindale, A., Martinez, E.,
Massey, E., Mawhinney, E., McLeod, M.P., Meador, K., Morgan, M., Morris, S.,
Miner, G., Miner, Z., Mitchell, T., Mohabbar, K., Morgan, M., Morris, S.,
Moser, M., Neal, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N.,
Nguyen, N., Nickerson, E., Nwokenwo, S., Ogun, M., Okunolu, G.,
Oregunye, N., Oviado, R., Pace, A., Payton, B., Peery, J., Perez, L.,
Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, Y.,
Rivers, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G.,
Scherrer, S., Scott, G., Shen, H., Shoohtari, N., Sison, I.,
Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H.,
Sutton, A., Swalek, A., Taber, P., Tameris, A., Tameris, K., Tang, H.,
Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S.,
Uman, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wang, Q.,
Wang, S., Ward-Moore, S., Warren, R., Washington, C., Watlington, S.,
Williams, G., Williamson, A., Wleczek, R., Wooten, S., Worley, K.,
Wu, C., Wu, Y., Wu, Y.F., Zhou, D., Zorrilla, S., Nelson, D.,
Weinstock, G. and Gibbs, R.

COMMENT Direct Submission
Unpublished
2 (bases 1 to 146568)
Worley, K.C.
Direct Submission
Submitted (19-MAR-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA

Center: Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Project Information
Center project name: AMEZ
Center clone name: CH224-57G3

Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 132495 bases at least Q40
Consensus quality: 137202 bases at least Q30
Consensus quality: 140042 bases at least Q20
Estimated insert size: 137866; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1456: contig of 1456 bp in length
1557 1556: gap of unknown length
2731 2731: contig of 1175 bp in length
2732 2831: gap of unknown length
2832 4180: contig of 1349 bp in length
4181 4280: gap of unknown length
4281 5835: contig of 1555 bp in length
5836 5935: gap of unknown length
5936 7358: contig of 1423 bp in length
7359 7459: gap of unknown length
7459 8616: contig of 1358 bp in length
8617 10936: contig of 2020 bp in length
8917 11036: gap of unknown length
10937 12381: contig of 1345 bp in length
11037 12382 12481: gap of unknown length
12382 15062: contig of 2581 bp in length
1482 15063 15162: gap of unknown length
15163 18933: contig of 3771 bp in length
18934 19033: gap of unknown length
19034 23106: contig of 4073 bp in length
23107 23206: gap of unknown length
23207 27707: contig of 4501 bp in length
27707 27807: gap of unknown length
27808 33059: contig of 5252 bp in length
33060 33159: gap of unknown length
33160 38669: contig of 5510 bp in length
38670 38769: gap of unknown length
38770 45346: contig of 6667 bp in length
45347 45536: gap of unknown length
45537 52247: contig of 6711 bp in length
52248 52347: gap of unknown length
52348 59244: contig of 6897 bp in length
59245 59344: gap of unknown length
59345 66497: contig of 7153 bp in length
66498 66597: gap of unknown length
66598 74127: contig of 7530 bp in length
74128 74227: gap of unknown length
74228 81722: contig of 7495 bp in length
81723 81822: gap of unknown length
81823 92875: contig of 11053 bp in length
92876 92975: gap of unknown length
92976 101243: contig of 8268 bp in length
101244 101343: gap of unknown length
101344 113869: contig of 12526 bp in length
113870 113969: gap of unknown length
113970 128447: contig of 14478 bp in length
128448 128547: gap of unknown length
128548 146568: contig of 18021 bp in length.

FEATURES
source 1. 146568
/organism="Apis mellifera"
/mol_type="genomic DNA"
/db_xref="taxon:7460"
/clone="CH224-57G3"

BASE COUNT 39316 a 30537 c 30943 g 39489 t 6283 others

ORIGIN

Query Match 76.2%; Score 16; DB 2; Length 146568;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGTCGACGTTGAGA 17
|||||
Db 135270 CGTCGACGTTGAGA 135255

RESULT 9
AC130730/c

LOCUS AC130730 166304 bp DNA linear HTG 14-AUG-2002
DEFINITION *Oryza sativa* (japonica cultivar-group) chromosome 5 clone P0681D04,
*** SEQUENCING IN PROGRESS ***; 6 ordered pieces.

ACCESSION AC130730
VERSION AC130730.1 GI:22218364
KEYWORDS HTG; HTGS PHASE2.
SOURCE
ORGANISM *Oryza sativa* (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; *Oryza*.
1 (bases 1 to 166304)
REFERENCE
AUTHORS
Chow, T.-Y., Hsing, Y.-I. C., Chen, C.-S., Chen, H.-H., Liu, S.-M.,
Chao, Y.-T., Chang, S.-J., Chen, H.-C., Chen, S.-K., Chen, T.-R.,
Chen, Y.-L., Cheng, C.-H., Chung, C.-I., Han, S.-Y., Hsiao, S.-H.,
Hsuing, J.-N., Hsu, C.-H., Huang, J.-J., Kau, P.-I., Lee, M.-C.,
Lien, H.-L., Li, Y.-F., Lin, S.-J., Lin, Y.-C., Wu, S.-W., Yu, C.-Y.,
Yu, S.-W., Wu, H.-P., and Shaw, J.-F.
Oryza sativa PAC P0681D04 genomic sequence

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Unpublished
2 (bases 1 to 166304)
Chow, T.-Y., and Hsing, Y.-I. C.
Direct Submission
Submitted (14-AUG-2002) Institute of Botany, Academia Sinica, 128,
Section 2, Academia Road, Nankang, Taipei 11529, Taiwan
* NOTE: This is a working draft sequence. It currently
* consists of 6 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

1 8678: contig of 8678 bp in length
8679 8779: gap of unknown length
8780 14903: contig of 6125 bp in length
14904 15003: gap of unknown length
15004 35393: contig of 20390 bp in length
35394 35494: gap of unknown length
35495 121324: contig of 85831 bp in length
121325 121424: gap of unknown length
121425 135356: contig of 13932 bp in length
135357 135456: gap of unknown length
135457 166304: contig of 30848 bp in length.

FEATURES
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="5"
/clone="P0681D04"

BASE COUNT 46182 a 37272 c 36481 g 45869 t 500 others

ORIGIN

Query Match 76.2%; Score 16; DB 2; Length 166304;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTTGAGATGA 20
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Db 99712 CGACGTTGAGATGA 99697

RESULT 10
AR268334 22 bp DNA linear PAT 10-APR-2003
LOCUS AR268334
DEFINITION Sequence 19 from patent US 6498148.
ACCESSION AR268334
VERSION AR268334.1 GI:29698684
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 22)
AUTHORS Raz,E.
TITLE Immunization-free methods for treating antigen-stimulated inflammation in a mammalian host and shifting the host's antigen immune responsiveness to a Th1 phenotype
JOURNAL Patent: US 6498148-A 19 24-DEC-2002;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
8 GAACGTCGAGATGA 22

Db

RESULT 11
AR287741
LOCUS AR287741 22 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6534062.
ACCESSION AR287741
VERSION AR287741.1 GI:31674761
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Raz,E., Cho,H.J., Richman,D. and Horner,A.A.
TITLE Methods for increasing a cytotoxic T lymphocyte response in vivo
JOURNAL Patent: US 6534062-A 1 18-MAR-2003;
FEATURES Location/Qualifiers
source 1..22
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BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
8 GAACGTCGAGATGA 22

Db

RESULT 12
AR287743
LOCUS AR287743 22 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 3 from patent US 6534062.
ACCESSION AR287743
VERSION AR287743.1 GI:31674763
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Raz,E., Cho,H.J., Richman,D. and Horner,A.A.
TITLE Methods for increasing a cytotoxic T lymphocyte response in vivo
JOURNAL Patent: US 6534062-A 3 18-MAR-2003;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
8 GAACGTCGAGATGA 22

Db

RESULT 13
AR308057
LOCUS AR308057 22 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6552006.
ACCESSION AR308057
VERSION AR308057.1 GI:31698950
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 22)
AUTHORS Raz,E., Kornbluth,R., Catanzaro,A., Hayashi,T. and Carson,D.
TITLE Immunomodulatory polynucleotides in treatment of an infection by an intracellular pathogen
JOURNAL Patent: US 6552006-A 1 22-APR-2003;
FEATURES Location/Qualifiers
source 1..22
/organism="unknown"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
8 GAACGTCGAGATGA 22

Db

RESULT 14
AX036945
LOCUS AX036945 22 bp DNA linear PAT 16-NOV-2000
DEFINITION Sequence 2 from Patent FR2790955.
ACCESSION AX036945
VERSION AX036945.1 GI:11226373
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Carpentier,A.
JOURNAL Patent: FR 2790955-A 2 22-SEP-2000;
ASSIST PUBL HOPITAUX DE PARIS (FR)
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
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/note="Oligodeoxynucleotide"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
8 GAACGTCGAGATGA 22

Db

RESULT 15
AX046993
LOCUS AX046993 22 bp DNA linear PAT 15-DEC-2000

DEFINITION Sequence 2 from Patent WO0067787.
ACCESSION AX046993
VERSION AX046993.1 GI:11876420
KEYWORDS
SOURCE
ORGANISM synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Moss, R.B.
TITLE Hiv immunogenic compositions and methods
JOURNAL Patent: WO 0067787-A 2 16-NOV-2000;
THE IMMUNE RESPONSE CORPORATION (US)
FEATURES
source
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="phosphorothioate-modified synthetic
oligodeoxynucleotide"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22
RESULT 16
AX083675 22 bp DNA linear PAT 28-FEB-2001
LOCUS AX083675
DEFINITION Sequence 1 from Patent WO0112223.
ACCESSION AX083675
VERSION AX083675.1 GI:13185407
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS van Nest, G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL sequences and compositions for use therein
DynaVax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic construct"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22
RESULT 17
AX083676 22 bp DNA linear PAT 28-FEB-2001
LOCUS AX083676
DEFINITION Sequence 2 from Patent WO0112223.
ACCESSION AX083676
VERSION AX083676.1 GI:13185408
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS van Nest, G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL sequences and compositions for use therein
Patent: WO 0112223-A 2 22-FEB-2001;
DynaVax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Synthetic construct"
BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22
RESULT 18
AX135650 22 bp DNA linear PAT 29-MAY-2001
LOCUS AX135650
DEFINITION Sequence 21 from Patent WO0132877.
ACCESSION AX135650
VERSION AX135650.1 GI:14271920
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Mackichan, M.L.
TITLE Cpg receptor (cpg-r) and methods relating thereto
JOURNAL Patent: WO 0132877-A 21 10-MAY-2001;
CHIRON CORPORATION (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Cpg oligonucleotide"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22
RESULT 19
AX148636 22 bp DNA linear PAT 08-JUN-2001
LOCUS AX148636
DEFINITION Sequence 1 from Patent WO0135991.
ACCESSION AX148636
VERSION AX148636.1 GI:14347254
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Tuck, S. and van Nest, G.
TITLE Immunomodulatory compositions containing an immunostimulatory
sequence linked to antigen and methods of use thereof

JOURNAL Patent: WO 0135991-A 1 25-MAY-2001;
Dynavax Technologies Corporation (US)
FEATURES
source
1. .22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="synthetic construct"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

RESULT 20
LOCUS AX148637 22 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 2 from Patent WO0135991.
ACCESSION AX148637
VERSION AX148637.1 GI:14347255
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Tuck,S. and van Nest,G.
TITLE Immunomodulatory compositions containing an immunostimulatory
JOURNAL Patent: WO 0135991-A 2 25-MAY-2001;
FEATURES
source
1. .22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="synthetic construct"
BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

RESULT 21
LOCUS AX250701 22 bp DNA linear PAT 06-OCT-2001
DEFINITION Sequence 1 from Patent WO0168078.
ACCESSION AX250701
VERSION AX250701.1 GI:15984439
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G.
TITLE Methods of suppressing hepatitis virus infection using
JOURNAL immunomodulatory polynucleotide sequences
Patent: WO 0168078-A 1 20-SEP-2001;
FEATURES
source
1. .22
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="synthetic construct"

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

RESULT 22
LOCUS AX250702 22 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 2 from Patent WO0168078.
ACCESSION AX250702
VERSION AX250702.1 GI:15984440
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G.
TITLE Methods of suppressing hepatitis virus infection using
JOURNAL immunomodulatory polynucleotide sequences
Patent: WO 0168078-A 2 20-SEP-2001;
FEATURES
source
1. .22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

RESULT 23
LOCUS AX252291 22 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 1 from Patent WO0168117.
ACCESSION AX252291
VERSION AX252291.1 GI:15985632
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G.
TITLE Methods of reducing papillomavirus infection using immunomodulatory
JOURNAL polynucleotide sequences
Patent: WO 0168117-A 1 20-SEP-2001;
FEATURES
source
1. .22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
|||||
8 GAACGTCGAGATGA 22

RESULT 24
AX252292 22 bp DNA linear PAT 05-OCT-2001
LOCUS Sequence 2 from Patent WO0168117.
ACCESSION AX252292
VERSION AX252292.1 GI:15985633
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G.
TITLE Methods of reducing papillomavirus infection using immunomodulatory polynucleotide sequences
JOURNML Patent: WO 0168117-A 2 20-SEP-2001;
FEATURES Dynavax Technologies Corporation (US)
source Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
|||||
8 GAACGTCGAGATGA 22

RESULT 25
AX252509 22 bp DNA linear PAT 05-OCT-2001
LOCUS Sequence 1 from Patent WO0168103.
ACCESSION AX252509
VERSION AX252509.1 GI:15985780
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G.
TITLE Methods of ameliorating symptoms of herpes infection using immunomodulatory polynucleotide sequences
JOURNML Patent: WO 0168103-A 1 20-SEP-2001;
FEATURES Dynavax Technologies Corporation (US)
source Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
|||||
8 GAACGTCGAGATGA 22

DB 8 GAACGTCGAGATGA 22

RESULT 26
AX252510 22 bp DNA linear PAT 05-OCT-2001
LOCUS Sequence 2 from Patent WO0168103.
ACCESSION AX252510
VERSION AX252510.1 GI:15985781
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G.
TITLE Methods of ameliorating symptoms of herpes infection using immunomodulatory polynucleotide sequences
JOURNML Patent: WO 0168103-A 2 20-SEP-2001;
FEATURES Dynavax Technologies Corporation (US)
source Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
|||||
8 GAACGTCGAGATGA 22

RESULT 27
AX252520 22 bp DNA linear PAT 05-OCT-2001
LOCUS Sequence 1 from Patent WO0168144.
ACCESSION AX252520
VERSION AX252520.1 GI:15985791
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G. and Tuck,S.
TITLE Biodegradable immunomodulatory formulations and methods for use thereof
JOURNML Patent: WO 0168144-A 1 20-SEP-2001;
FEATURES Dynavax Technologies Corporation (US)
source Location/Qualifiers
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
|||||
8 GAACGTCGAGATGA 22

RESULT 28
AX252521

LOCUS AX252931 22 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 2 from Patent WO0168144.
ACCESSION AX252931
VERSION AX252931.1 GI:15985792
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G. and Tuck,S.
TITLE Biodegradable immunomodulatory formulations and methods for use thereof
JOURNAL Patent: WO 0168144-A 2 20-SEP-2001;
Dynamax Technologies Corporation (US)
FEATURES
SOURCE 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22
RESULT 29
LOCUS AX252934 22 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 1 from Patent WO0168143.
ACCESSION AX252934
VERSION AX252934.1 GI:15986201
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G. and Tuck,S.
TITLE Immunomodulatory formulations and methods for use thereof
JOURNAL Patent: WO 0168143-A 1 20-SEP-2001;
Dynamax Technologies Corporation (US)
FEATURES
SOURCE 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22
RESULT 30
LOCUS AX252935 22 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 2 from Patent WO0168143.
ACCESSION AX252935
VERSION AX252935.1 GI:15986202
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van Nest,G. and Tuck,S.
TITLE Immunomodulatory formulations and methods for use thereof
JOURNAL Patent: WO 0168143-A 2 20-SEP-2001;
Dynamax Technologies Corporation (US)
FEATURES
SOURCE 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22
RESULT 31
LOCUS AX253113 22 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 1 from Patent WO0168116.
ACCESSION AX253113
VERSION AX253113.1 GI:15986281
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G.
TITLE Methods of preventing and treating respiratory viral infection usi
ng immunomodulatory polynucleotide sequences
JOURNAL Patent: WO 0168116-A 1 20-SEP-2001;
Dynamax Technologies Corporation (US)
FEATURES
SOURCE 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22
RESULT 32
LOCUS AX253114 22 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 2 from Patent WO0168116.
ACCESSION AX253114
VERSION AX253114.1 GI:15986282
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest,G.
TITLE Methods of preventing and treating respiratory viral infection usi
ng immunomodulatory polynucleotide sequences

JOURNAL Patent: WO 0168116-A 2 20-SEP-2001;
DynaVax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGCAGATGA 20
|||||
8 GAACGTTGCAGATGA 22

RESULT 33
AX253123 22 bp DNA linear PAT 05-OCT-2001
LOCUS Sequence 1 from Patent WO0168077.
DEFINITION AX253123
ACCESSION AX253123.1 GI:15986291
VERSION
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest, G.
TITLE Methods of preventing and treating viral infections using immunomodulatory polynucleotide sequences
JOURNAL Patent: WO 0168077-A 1 20-SEP-2001;
DynaVax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGCAGATGA 20
|||||
8 GAACGTTGCAGATGA 22

RESULT 34
AX253124 22 bp DNA linear PAT 05-OCT-2001
LOCUS Sequence 2 from Patent WO0168077.
DEFINITION AX253124
ACCESSION AX253124
VERSION AX253124.1 GI:15986292
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS van Nest, G.
TITLE Methods of preventing and treating viral infections using immunomodulatory polynucleotide sequences
JOURNAL Patent: WO 0168077-A 2 20-SEP-2001;
DynaVax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"

/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 4 c 7 g 5 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGCAGATGA 20
|||||
8 GAACGTTGCAGATGA 22

RESULT 35
AX468499 22 bp DNA linear PAT 16-JUL-2002
LOCUS Sequence 19 from Patent WO0226209.
DEFINITION AX468499
ACCESSION AX468499
VERSION AX468499.1 GI:21901329
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS O'Hagan, D., Otten, G., Donnelly, J. J., Polo, J. M., Barnett, S., Singh, M., Ulmer, J., and Dubensky, T. W.
TITLE Microparticles for delivery of the heterologous nucleic acids
JOURNAL Patent: WO 0226209-A 19 04-APR-2002;
CHIRON CORPORATION (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Artificial sequence is synthesized"

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGCAGATGA 20
|||||
8 GAACGTTGCAGATGA 22

RESULT 36
AX592312 22 bp DNA linear PAT 27-JAN-2003
LOCUS Sequence 2 from Patent WO02052002.
DEFINITION AX592312
ACCESSION AX592312
VERSION AX592312.1 GI:27950414
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon, K. L., and Dina, D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 2 04-JUL-2002;
DynaVax Technologies Corporation (US)
FEATURES
source
1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
 |||||
 Db 8 GAACGTCGAGATGA 22

RESULT 37
 AX592332 22 bp DNA linear PAT 27-JAN-2003
 LOCUS Sequence 12 from Patent WO02052002.
 AX592332
 ACCESSION AX592332
 VERSION AX592332.1 GI:27950424
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 FEATURES
 1
 REFERENCE
 1 Fearon,K.L. and Dina,D.
 TITLE Immunomodulatory polynucleotides and methods of using the same
 JOURNAL Patent: WO 02052002-A 12 04-JUL-2002;
 Dynavax Technologies Corporation (US)
 Location/Qualifiers
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 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Polynucleotide containing CG"

BASE COUNT 5 a 4 c 7 g 6 t
 ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
 |||||
 Db 8 GAACGTCGAGATGA 22

RESULT 38
 AX592332 22 bp DNA linear PAT 27-JAN-2003
 LOCUS Sequence 22 from Patent WO02052002.
 AX592332
 ACCESSION AX592332
 VERSION AX592332.1 GI:27950434
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 FEATURES
 1
 REFERENCE
 1 Fearon,K.L. and Dina,D.
 TITLE Immunomodulatory polynucleotides and methods of using the same
 JOURNAL Patent: WO 02052002-A 22 04-JUL-2002;
 Dynavax Technologies Corporation (US)
 Location/Qualifiers
 1..22
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Polynucleotide containing CG"

BASE COUNT 4 a 6 c 6 g 6 t
 ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTGGA 15
 |||||
 Db 1 TCGTGAACGTTGGA 15

RESULT 39
 AX592350 22 bp DNA linear PAT 27-JAN-2003
 LOCUS Sequence 40 from Patent WO02052002.
 AX592350
 ACCESSION AX592350
 VERSION AX592350.1 GI:27950452
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 FEATURES
 1
 REFERENCE
 1 Fearon,K.L. and Dina,D.
 TITLE Immunomodulatory polynucleotides and methods of using the same
 JOURNAL Patent: WO 02052002-A 40 04-JUL-2002;
 Dynavax Technologies Corporation (US)
 Location/Qualifiers
 1..22
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Polynucleotide containing CG"

BASE COUNT 6 a 3 c 7 g 6 t
 ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
 |||||
 Db 8 GAACGTCGAGATGA 22

RESULT 40
 AX592355 22 bp DNA linear PAT 27-JAN-2003
 LOCUS Sequence 45 from Patent WO02052002.
 AX592355
 ACCESSION AX592355
 VERSION AX592355.1 GI:27950457
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 FEATURES
 1
 REFERENCE
 1 Fearon,K.L. and Dina,D.
 TITLE Immunomodulatory polynucleotides and methods of using the same
 JOURNAL Patent: WO 02052002-A 45 04-JUL-2002;
 Dynavax Technologies Corporation (US)
 Location/Qualifiers
 1..22
 /organism="synthetic construct"
 /mol_type="genomic DNA"
 /db_xref="taxon:32630"
 /note="Polynucleotide containing CG"

BASE COUNT 5 a 2 c 7 g 2 others
 ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 22;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
 |||||
 Db 8 GAACGTCGAGATGA 22

RESULT 41

AX592356
LOCUS AX592356 22 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 46 from Patent WO02052002.
ACCESSION AX592356
VERSION AX592356.1 GI:27950458
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon, K.L. and Dina, D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 46 04-JUL-2002;
Dynavax Technologies Corporation (US)
FEATURES
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
misc_feature 5
/note="n = 5-bromocytosine"
BASE COUNT 5 a 3 c 7 g 6 t 1 others
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22

RESULT 42
LOCUS AX592369 22 bp DNA linear PAT 27-JAN-2003
DEFINITION Sequence 59 from Patent WO02052002.
ACCESSION AX592369
VERSION AX592369.1 GI:27950471
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon, K.L. and Dina, D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 59 04-JUL-2002;
Dynavax Technologies Corporation (US)
FEATURES
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22

RESULT 43
LOCUS AX720306 22 bp DNA linear PAT 15-APR-2003
DEFINITION Sequence 1 from Patent WO03000332.
ACCESSION AX720306
VERSION AX720306.1 GI:29892140

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Barenholz, Y., Kedari, E., Louria-Hayon, Y., Joseph, A., Raz, E. and Takabayashi, K.
TITLE Method for preparation of vesicles loaded with immunostimulatory oligodeoxynucleotides
JOURNAL Patent: WO 03000332-A 1 03-JAN-2003;
Viesum Research Development Company of the Hebrew Univ of Jerusalem (IL); The Regents of the University of California (US)
FEATURES
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22

RESULT 44
LOCUS BD009235 22 bp DNA linear PAT 31-JAN-2002
DEFINITION Immunostimulatory polynucleotide/immunomodulatory molecule conjugates.
ACCESSION BD009235
VERSION BD009235.1 GI:18637608
KEYWORDS JP 2001503254-A/34.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 22)
AUTHORS Carson, D.A., Raz, E. and Roman, M.
TITLE Immunostimulatory polynucleotide/immunomodulatory molecule
JOURNAL Patent: JP 2001503254-A 34 13-MAR-2001;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT OS Artificial Sequence
PN JP 2001503254-A/34
PD 13-MAR-2001
PF 09-OCT-1997 JP 1998518649
PI 11-OCT-1996 US 60/028118
PI DENNIS A CARSON, EYAL RAZ, MARK ROMAN
PC A61K39/00, A61K39/385, A61K39/39
CC
FH key Location/Qualifiers
FT source 1..22
/organism="Artificial Sequence".
FEATURES
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22

RESULT 45
BD182369 22 bp DNA linear PAT 15-MAY-2003
LOCUS Anti-tumor antigens or their epitopes against HTLV-1 tumor.
ACCESSION BD182369
VERSION BD182369.1 GI:30793287
KEYWORDS WO 02090981-A/1.
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 22)
AUTHORS Hanabuchi,S., Ohashi,T. and Kannagi,M.
TITLE Anti-tumor antigens or their epitopes against HTLV-1 tumor
JOURNAL Patent: WO 02090981-A 1 14-NOV-2002;
JAPAN SCIENCE AND TECHNOLOGY CORP, SHINO HANABUCHI, TAKASHI OHASHI,
MARI KANNAGI
COMMENT OS Artificial Sequence
PN WO 02090981-A/1
PD 14-NOV-2002
PF 02-MAY-2002 WO 2002JP004406
PR 08-MAY-2001 JP 01P 137526
PI SHINO HANABUCHI, TAKASHI OHASHI, MARI KANNAGI
PC GOIN33/50, GOIN33/15, A6IK39/00
CC Description of Artificial Sequence: ISS-ODN
FT Key Location/Qualifiers
FT source 1..22
FEATURES Location/Qualifiers
source 1..22
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 6 a 3 c 7 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GAACGTTGAGATGA 20
Db 8 GAACGTTGAGATGA 22
RESULT 46
AX083677/c 23 bp DNA linear PAT 28-FEB-2001
LOCUS AX083677
DEFINITION Sequence 3 from Patent WO0112223.
ACCESSION AX083677
VERSION AX083677.1 GI:13185409
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van Neeft,G.
TITLE Methods of modulating an immune response using immunostimulatory s
JOURNAL enquences and compositions for use therein
Dynamax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic construct"
BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTGAGATGA 20
Db 15 GAACGTTGAGATGA 1
RESULT 47
AX148638 23 bp DNA linear PAT 08-JUN-2001
LOCUS AX148638/c
DEFINITION Sequence 3 from Patent WO0135991.
ACCESSION AX148638
VERSION AX148638.1 GI:14347256
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Tuck,S. and van Neeft,G.
TITLE Immunomodulatory compositions containing an immunostimulatory
JOURNAL sequence linked to antigen and methods of use thereof
Dynamax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1..23
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic construct"
BASE COUNT 6 a 8 c 3 g 6 t
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Query Match 71.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GAACGTTGAGATGA 20
Db 15 GAACGTTGAGATGA 1
RESULT 48
AX250703 23 bp DNA linear PAT 05-OCT-2001
LOCUS AX250703/c
DEFINITION Sequence 3 from Patent WO0168078.
ACCESSION AX250703
VERSION AX250703.1 GI:15984441
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS van Neeft,G.
TITLE Methods of suppressing hepatitis virus infection using
JOURNAL immunomodulatory polynucleotide sequences
Dynamax Technologies Corporation (US)
FEATURES Location/Qualifiers
source 1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GAACGTTGAGATGA 20
Db 15 GAACGTTGAGATGA 1
RESULT 49

AX252293/c
LOCUS AX252293 23 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 3 from Patent WO0168117.
ACCESSION AX252293
VERSION AX252293.1 GI:15985634
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
van Nest, G.
TITLE
Method of reducing papillomavirus infection using immunomodulatory polynucleotide sequences
JOURNAL
Patent: WO 0168117-A 3 20-SEP-2001;
DynaVax Technologies Corporation (US)
FEATURES
source
1..23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
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Db 15 GAACGTCGAGATGA 1
RESULT 50
AX252511/c
LOCUS AX252511 23 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 3 from Patent WO0168103.
ACCESSION AX252511
VERSION AX252511.1 GI:15985782
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
van Nest, G.
TITLE
Methods of ameliorating symptoms of herpes infection using immunomodulatory polynucleotide sequences
JOURNAL
Patent: WO 0168103-A 3 20-SEP-2001;
DynaVax Technologies Corporation (US)
FEATURES
source
1..23
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/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
|||||
Db 15 GAACGTCGAGATGA 1
RESULT 51
AX252522/c
LOCUS AX252522 23 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 3 from Patent WO0168144.
ACCESSION AX252522
VERSION AX252522.1 GI:15985793

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
van Nest, G. and Tuck, S.
TITLE
Biodegradable immunomodulatory formulations and methods for use thereof
JOURNAL
Patent: WO 0168144-A 3 20-SEP-2001;
DynaVax Technologies Corporation (US)
FEATURES
source
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/organism="synthetic construct"
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/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
|||||
Db 15 GAACGTCGAGATGA 1
RESULT 52
AX252936/c
LOCUS AX252936 23 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 3 from Patent WO0168143.
ACCESSION AX252936
VERSION AX252936.1 GI:15986203
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
van Nest, G. and Tuck, S.
TITLE
Immunomodulatory formulations and methods for use thereof
JOURNAL
Patent: WO 0168143-A 3 20-SEP-2001;
DynaVax Technologies Corporation (US)
FEATURES
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/note="Polynucleotide containing CG"
BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN
Query Match 71.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
|||||
Db 15 GAACGTCGAGATGA 1
RESULT 53
AX253115/c
LOCUS AX253115 23 bp DNA linear PAT 05-OCT-2001
DEFINITION Sequence 3 from Patent WO0168116.
ACCESSION AX253115
VERSION AX253115.1 GI:15986283
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS
van Nest, G.

TITLE Methode of preventing and treating respiratory viral infection using immunomodulatory polynucleotide sequences
JOURNAL Patent: WO 0168116-A 3 20-SEP-2001;
DynaVax Technologies Corporation (US)
FEATURES Location/Qualifiers
SOURCE 1. 23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GAACGTCGAGATGA 20
15 GAACGTCGAGATGA 1

RESULT 54
AX253125/c 23 bp DNA linear PAT 05-OCT-2001
LOCUS Sequence 3 from Patent WO0168077.
DEFINITION AX253125
ACCESSION AX253125
VERSION AX253125.1 GI:15986293
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS van Nest, G.
JOURNAL Method of preventing and treating viral infections using immunomodulatory polynucleotide sequences
Patent: WO 0168077-A 3 20-SEP-2001;
DynaVax Technologies Corporation (US)
FEATURES Location/Qualifiers
SOURCE 1. 23
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 6 a 8 c 3 g 6 t
ORIGIN

Query Match 71.4%; Score 15; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GAACGTCGAGATGA 20
15 GAACGTCGAGATGA 1

RESULT 55
AE007311 11033 bp DNA linear BCT 15-AUG-2001
LOCUS Sinorhizobium meliloti plasmid pSymba section 117 of 121 of the complete plasmid sequence.
DEFINITION AE007311 AE006469
ACCESSION AE007311
VERSION AE007311.1 GI:14524427
KEYWORDS
SOURCE
ORGANISM
Sinorhizobium meliloti (Rhizobium meliloti)
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
1 (bases 1 to 11033)
Barnett, M.J., Fisher, R.F., Jones, T., Komp, C., Abola, A.P., Gurjal, M., Hong, A., Huitzer, L., Capela, D., Galibert, F., Gouzy, J., Kaiman, S., Keating, D.H., Palm, C., Peck, M.C., Surzycki, R., Kalman, S., Keating, D.H., Palm, C., Peck, M.C., Surzycki, R.,

TITLE Wells, D.H., Yeh, K.-C., Davis, R.W., Federspiel, N.A. and Long, S.R. Nucleotide sequence and predicted functions of the entire Sinorhizobium meliloti pSymba megaplasmid
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 98 (17), 9883-9888 (2001)
MEDLINE 21396509
PUBMED 11481432
AUTHORS
REFERENCE 2 (bases 1 to 11033)
Barnett, M.J., Fisher, R.F., Jones, T., Komp, C., Abola, A.P., Gurjal, M., Hong, A., Huitzer, L., Capela, D., Galibert, F., Gouzy, J., Kaiman, S., Keating, D.H., Palm, C., Peck, M.C., Surzycki, R., Wells, D.H., Yeh, K.-C., Davis, R.W., Federspiel, N.A. and Long, S.R. Direct Submision
Submitted (29-MAR-2001) Biological Sciences, Stanford University, 371 Serra Mall, Stanford, CA 94305, USA
FEATURES Location/Qualifiers
SOURCE 1. 11033
/organism="Sinorhizobium meliloti"
/mol_type="genomic DNA"
/strain="1021"
/db_xref="taxon:382"
/plasmid="pSymba"
/gene="Sma2337"
167. 1462
167. 1462
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TLAIGNAVGVSGIALGVIGGTLTLVLFHKIGMPTLLVACSLPLVAAIMKDDRA
VASPEAPLRRASLFGPRRNAMMILAPLTVASRGIVAGMGSVLYVSKVPTW
GYMSGAAATKGLIALIALITRKAGITRTLLIGLRISCTFLPALNAGCIPGTA
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/function="Cell processes; Transport of small molecules; incorporation metal ions"
/note="Glimmer prediction; identical to Rhba (rhba) from Sinorhizobium meliloti, AA009412, Q923R2; aminotransferase class-III-pyridoxal phosphate family; rhizobactin siderophore biosynthesis pathway"
/codon_start=1
/transl_table=1
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/protein_id="AAK65916.1"
/db_xref="GI:14524429"
/translation="MPADLAARTSYKIFNGVDLMDASARADNAFYLDROERRESNARS
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VTFRGATHGMSQSLISLGSIGPPKASVQGLVFGAFPPFYPAAYCPRGCGNERTATLA
AVEFRALRDEBGSINRPAVALLEAVOGEGVLPAPVEMLAVRVRTRDLCITPLIVDS
VQSGVAGRTSGFYAKGIIIPDVVLLSKAIGGGLPLVVIYREBLDLMKPPAHAGTFR
GNOLMAAGSKTLEIIERERLVERAAIAGRLRANLERIAOQTPYIGVREGGMLGV
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2931. 4418
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gene

CDS

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incorporation metal ions"
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L-2,4-diaminobutyrate decarboxylase, RhsB (RhbB), from
Sinorhizobium meliloti, AAD09413; pyridoxal-dependent
decarboxylase family; rhizobactin siderophore biosynthesis
family"
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GNFTSGTOSNMNTALYLAARCGDPARKAGVLTSAHAFSIRKSAALIGFEDAVIA
IAADGRMSVPALKARELRVAGBGRIPAVAVAGTDDGAIIDPLVELADAAQNV
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Sinorhizobium meliloti; Q9Z3R0, AAD09414"
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protein"
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EASRRYSSEPAAPLRFWFAVESLFTFHGSGSPAAEMLKEMAGSDIDALKPLP
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MKMSIGVGTITSYVNLARELRGDGMYRFRRLHMDQFSRYGTLTIPPAKGV
KIDGALIDGLSVSMENPFTGANADNVSLAACHLDPDRSRLGALIRNAHLERR
PLDIVARDWFERFLTIIVRPILGLYLRHIGAMEAQNVIEHGYPGLGYRNOG
PFHHERAGALVEALPGFGEPSVSEVGEVDERLIYAFINSVGMALGREGVLS
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6155..6745
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incorporation metal ions"
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Sinorhizobium meliloti, Q9Z3Q9, AF110737"
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protein"
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/db_xref="GI:14524432"
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AHVPOWKAKAPLIDIAIYIDINLADPHQDPIYGLIDGPMVWEVYAKDVLRVY
PAEKDRGCHMLVGESFPGRGIAIPVITAFTRFLFDPRGQKVGESVYAKRULR
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6742..8112
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incorporation metal ions"
/note="glimmer prediction; identical to RhbE (RhbE) from
Sinorhizobium meliloti, Q9Z3Q8, AAD09416"
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protein"
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EGLLIPGTLLOVPFMADLVMTADPTHRSLFNTYLAVDRLTKFYFENFMIPROEDYH
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LPKMAOITKTLALMHSSRFGRRLIESRRRVTVIGSGQSAACVLLALNDTPEMA
AGASIQMTTRAGCFPMESYKLGIEFYTPDMRPHRAPRAREIYADQGLYKGIS
FSTIGELFDLWYERSVGGDRGLLFSNCAVETLESAGSGSPFIRGINHNLDEKATV
ETFDIAVATGVRHAMPEWLGSLKGSVLDTCMGDLVVGDFRRARSDDGKHVYONA
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8096..9901
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incorporation metal ions"
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RIGGYSOYLAFPTBNRTPTEVRLTGUSKEKRSATBETTLNBEGLVRAVAVSPSP
CAKLAARGSVDTHTMPEHPWQMDHIVHPADADIAHGHTVFLGKGDLYLPQOSVR
TLSNHSPEKSTLKCMTILMTAVYRGIPIGRALTAALCTTWLQDLARDQFLSEBCG
71.4%; Score 15; DB 1; Length 11033;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTGAACGTTGGA 15
DB 3991 TCGTGAACGTTGGA 4005
RESULT 56
AF110737 11853 bp DNA linear BCT 03-APR-2001
LOCUS Sinorhizobium meliloti strain 2011 rhizobactin regulon, complete
DEFINITION sequence.
ACCESSION AF110737
VERSION AF110737.1 GI:4151930
KEYWORDS Sinorhizobium meliloti (Rhizobium meliloti)
ORGANISM Sinorhizobium meliloti
REFERENCE 1. Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
AUTHORS Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
1 Lynch,D., O'Brien,J., Welch,T., Clarke,P., Cui,Y,P.O., Crosa,J.H.
TITLE Genetic organization of the region encoding regulation,
biosynthesis, and transport of rhizobactin 1021, a siderophore
produced by Sinorhizobium meliloti
J. Bacteriol. 183 (8), 2576-2585 (2001)
JOURNAL MEDLINE 21172875
MEDLINE 11274118
REFERENCE 2 (bases 1 to 11853)
AUTHORS Lynch,D., O Connell,M. and O'Brien,J
TITLE Cloning and sequence analysis of the Sinorhizobium meliloti 2011

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rhizobactin regulon
3 (bases 1 to 11853)
Lynch,D., O Connell,M. and O'Brien,J.
Direct Submission
Submitted (03-DEC-1998) School of Biotechnology, Dublin City
University, Glasnevin, Dublin, Leinster Dublin 9, Ireland
Location/Qualifiers
1. 11853
/organism="Sinorhizobium meliloti"
/mol_type="Genomic DNA"
/strain="2011"
/db_xref="taxon:382"
8. 11848
/gene="rhizobactin regulon"
9. 26
/gene="rhizobactin regulon"
/note="FUR Binding Site"
42. 1454
/gene="rhba"
/note="previously rhaa"
42. 1454
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/note="similar to DABA aminotransferase"
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/db_xref="GI:4151931"
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VSEFARLHMGQSLSLMGSPKASVQLPVGAFFPYAVRCFPERGNETATTLA
AVERALRDGEGGINRPAVILAVQEGVTPAVEMLRVRRVTDLGIPLIVDE
VQSGVGTSGFYAFQKAGIIPDVVLSKAIIGGLPLAVIYREDLMLPGAHGTFR
GNOLAMAGSKTLEIIEERILVERAIIAGRRIRANLRIIAOTPIYIGVSGSGMLGV
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IDVSGALAAAPERLGRKA"
1451. 2938
/gene="rhbb"
/note="previously rhab"
1451. 2938
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/function="siderophore biosynthesis"
/note="similar to DABA decarboxylase"
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/protein_id="AAD09413.1"
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IAAADGMSVPALKAELRVAGBGRIPVAVATGTTDLGAIQDPLVEIADLAANQV
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ASKADYLNPEDAVADAPNLVERSMQTRRADALKIIMTMARIGDGDALICQTLON
THAAAEVATREYELIAGPSPSLSTVLFYVSGARGFADAITLKTFRALLFNAGIAALA
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2925. 4682
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BASRRYSPEPRLAAGPELPAVASEGLPHHTGSGSPASAEMLKRAMSDIDALKAFLP
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MLKSLDVGITNSVRVNLARELDGDMYRFRRLHWQDFRSYFGLLTLPDPAWGV
KIDALIDGLSVSMRENPFGANADRVNRLAACEHLPDGSRILGALIRRAHLER
PLDIVADWFERPLTIFVRPIFGLYLHGHIMEARQONIIVEIHHGVDI GLFYDNOG
PFHERRAHGALVEALPGFSEPSVFGSEVPDERLLYAFINSYLGAMVGALEGLVS
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/db_xref="GI:4151935"
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LILPFTLQVPMADLVTMADPHTRLSPNTLAVHDLRYKFEYENFPIPOEDHYC
RMAEQOLSAQCFGEVVDVAHESASDSFTVESRASGQKQOGRSNTAIGVTAPFLP
KMAQIKTLAPLMHSSSEFRRLLELSKRRVTVVIGSGSAECVATLADGLLPGVAVAG
ASIQWITRSAGFPMEYSKGLIYEPTDYMGHFRILPVRRREIVADQGLLYKGISFS
TIGEIFDLMYRSYVSGRDPGLAFNSNAVETLSAGSGSFRIGINNHILDEKATVET
DAIVAAATGYRHAMPWMLGSLKSVLDTCEMDLVYGGDFRRARSDGKGHYFYQNAET
FHHGVGAPDGLGAFRNAVIVNQLGRBHYRVNASASFQKGLPSSQTPASSISGDFY
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6616. 8421
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/note="similar to Iucc"
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KPGHVRIDIDELQVRFKARYVPDNLSDVDAAPLRKGNSSAPLPHDPLAPCAEVLPLK
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RIGQYSDYLAFTPEBNTPTFVLMVGSKEKASFTAEETLVBGLVREAVGSFESF
CAKLAARGGSVDTHYMPVHPWMDHMI VPHFADIAAGHIVFLGKDDLYLPQOSVR
TLSNISHPEKSTLKCMTIINTAVYRGIPGRALTAAPLTTMLDQLARDOFLSEBEG
LVLLGSRAGHYVVPQSTIEGAPYOFNMGCMWRDLSAHLKSGSTGLPALLHA
GTGCKPVALOALAKSGMTVSWKARLDVVI PVPHILAKHGLAFSAAGNATYILKN
GRPRRLARDFIDPIVDODAFPSATLAVPFRVAVVLCPADPLIHITQTLPTCYVR
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complement (8495. 9439)

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/protein_id="AAD09418.1"
/db_xref="GI:4151937"
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TNAGVILROEYSEEHAGMVAFYDLPLVLAODIGNVSPRETPHNMASIKMVEQ
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9608..11848
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/transl_table=11
/product="TonB-dependent siderophore receptor Rhra"
/protein_id="AAD09419.1"
/db_xref="GI:4151938"
/translation="MGNNGSGISFCVFVVVIGFTGAVAOEPANOSBAVTSLEIIV
TCGRSAOOISIAITIVYVNDPOIOEARSGETLQOIGETIPSPDASDGRATFGQ
NLRGRPLIVGVSGMNSARSLRPFDAIDPENIRVAVLSGATAIYGGNATGIIINI
ITRKGDAEPGLHAETVGTGMSGSGFASQDPDNAGATYNSENNDAISLSTAGNTGA
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Query Match
Best Local Similarity 71.4%; Score 15; DB 1; Length 11853;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGACGTTGCA 15
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Db 2511 TCGTCGACGTTGCA 2525

RESULT 57
AF381613 18662 bp DNA linear INV 31-JAN-2002
LOCUS Ancylostoma caninum metalloendopeptidase-1 (MEP-1) gene, partial
DEFINITION
ACCESSION AF381613 GI:14549936
VERSION
KEYWORDS
SOURCE Ancylostoma caninum (dog hookworm)
ORGANISM Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.
REFERENCE 1 (bases 1 to 18662)
AUTHORS Jones,B.F. and Hotez,P.J.
TITLE Molecular cloning and characterization of Ac-mep-1, a
developmentally regulated gut luminal metalloendopeptidase from
adult Ancylostoma caninum hookworms
JOURNAL Mol. Biochem. Parasitol. 119 (1), 107-116 (2002)
MEDLINE 21620013
PUBMED 11755191
REFERENCE 2 (bases 1 to 18662)
AUTHORS Jones,B.F. and Hotez,P.J.
TITLE Direct Submission
JOURNAL Submitted (17-MAY-2001) Department of Epidemiology and Public
Health, Yale University School of Medicine, 60 College St., New
Haven, CT 06510, USA
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/db_xref="taxon:29170"

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SFQYLRHNNATDIGNRIGTKYDAODDVNAEIVALEVNVSDTKMSETEBLVATLIF
TCVHTTRAKRDIKNSKNVLIEMRDLFGIGIPRLNLTKKDIDFDMCKFEQNHMGTL
LGNVSVDFKRVKNGSLFISQPIYMAARDPVFVFQTHKQENRVSILNSVRSFAKIV
LDSPSPYLDMSRSARDVVKLEQVIAASAKFESLRNVAQOHNRTIDQLPAKPAIK
WDSYFKALLSTSVQGVDDNNKONIILTOPSYFQMLNALPFGADDDRTIANYLVLHIOE
ADPFGALKTSGVQSDVYPALIRKGKVTGVRGOOLTRSHDPTVEDANIOCLNSMTYM
PFGGYVVKRKRNDVDVKDIEHOTELVFNPF"
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Query Match
Best Local Similarity 71.4%; Score 15; DB 3; Length 18662;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GACGTTGAGATGA 20
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Db 10678 GACGTTGAGATGA 10692

RESULT 58
AC013960/c 83321 bp DNA linear HTG 16-NOV-1999
LOCUS Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***
DEFINITION
ACCESSION AC013960 GI:6437375
VERSION
KEYWORDS HTG; HTGS_PHASE2
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 83321)
AUTHORS Adams,M. and Venter,J.C.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
COMMENT This sequence was identified as CDM:10210347 by the submitter.
For further information on this sequence e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
source location/Qualifiers
1..83321
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"

BASE COUNT 22661 a 18791 c 19196 g 22673 t
ORIGIN


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Query Match          71.4%; Score 15; DB 2; Length 83321;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      79322 TCGTCGAACGTTGCA 79308

RESULT 59
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LOCUS      Cyanidium caldarium strain Rkl chloroplast, complete genome.
DEFINITION
ACCESSION  AF022186.2 GI:6466296
VERSION     AF022186.2 GI:6466296
KEYWORDS
SOURCE      chloroplast Cyanidium caldarium
            Cyanidium caldarium
            Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales;
            Porphyridiaceae; Cyanidium.
REFERENCE   1 (bases 130696 to 132364)
AUTHORS     Vogel,H., Fischer,S. and Valentini,K.
TITLE       A model for the evolution of the plastid sec apparatus inferred
            from secY gene phylogeny
JOURNAL     Plant Mol. Biol. 32 (4), 685-692 (1996)
MEDLINE     8980520
PUBMED
REFERENCE   2 (bases 1 to 164921)
AUTHORS     Gloeckner,G., Rosenthal,A. and Valentini,K.
TITLE       The structure and gene repertoire of an ancient red algal plastid
            genome
JOURNAL     J. Mol. Evol. 51 (4), 382-390 (2000)
MEDLINE     10496959
PUBMED
REFERENCE   3 (bases 46857 to 47851)
AUTHORS     Valentini,K.
TITLE       Direct Submision
JOURNAL     Submitted (22-MAR-1996) Institute for Plant Physiology, Justus
            Liebig University, Heinrich Buff Ring 58-62, Giessen 55392, Germany
4 (bases 28701 to 75580)
AUTHORS     Gloeckner,G., Rosenthal,A. and Valentini,K.
TITLE       Direct Submision
JOURNAL     Submitted (02-SEP-1997) Department of Genome Analysis, IMB Jena,
            Beutenbergstr. 11, Jena 07745, Germany
5 (bases 1 to 164921)
AUTHORS     Gloeckner,G., Rosenthal,A. and Valentini,K.
TITLE       Direct Submision
JOURNAL     Submitted (18-NOV-1999) Genome Analysis, Institute for Molecular
            Biotechnology, Beutenbergstrasse 11, Jena 07745, Germany
6 (bases 130696 to 132364)
AUTHORS     Vogel,H., Fischer,S. and Valentini,K.
TITLE       Direct Submision
JOURNAL     Submitted (18-NOV-1999) Institute for Plant Physiology, Justus
            Liebig University, Heinrich Buff Ring 58-62, Giessen 55392, Germany
On or before Nov 23, 1999 this sequence version replaced gi:529651,
gi:1240002, gi:2465730.

FEATURES             location/Qualifiers
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                     /strain="Rkl"
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     repeat_unit     repeat unit separated by stem loop"
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                     /note="stem-loop separates direct repeat unit"
     stem_loop       580..780
                     /note="similar to yeast mitochondrial origin of
                     replication region in GenBank Accession Number J36902"
     rep_origin      986..2041
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LGSASWFPAPSGVAAI FRLFLPGFPHMTLNFPHMGVAGIIGALLCAIHATVE
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LVILKALFTGGIYDTMAFGGDIRFTNPPLNPAI IFSYLLKSPFGSEGVTVGVNNE
DVIGIHWIGTVCVIGIWHILTRPFSGARRAFWMSGAYLSGILGALMGOTPAEY
AMWNNTVYPSSEFVGPPTAAESAOAFTLVVDORLGANIASOTGPTGKXKMSPTG
EVLIGETMRFMWDLRAPMLEPLRBSNGLDINKINDIOPQERRAAAEVMTAIPGSLN
SVGCVATRINSVNVYSRSMTTSHFLGFTIFIGHLMHAGRAAAAAGFKGNREN
EPVLSMRPLD"
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LSQSDPYLNFHGVPPSPGLGIDSPITIGTILIDIFTEILSRQLKPL"
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    TLGRIENVLIGSEIDKGPVINSKLPVIRPAKFTQLETKSIFETGJLDLAPR
    RGKIGLFGAGVGTVMIMELINNVAHAGSVGAGVGEERTREGNDLYOMKESGV
    INEKDINSKVALCYGOMNEPRGARMYGLTALMAEYRDVYKONVLEFDINRFSV
    QAGSEVALGEMSPSANGQPTLGTENKALQORITSTLDGTSISQAVYVPADDLTDP
    APATFAHDATTVLSRALAKGTPVADPELDSITMLOPGIVSDEHTTARKKETL
    ORYKELQDIALIGDELSEEDRLIVASRAKIEKPLSOPFEVAEVTGISGRYVSLD
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    7 AACGTTGAGATGAT 21
    DB
    113665 AACGTTGAGATGAT 113679

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Query Match. 71.4%; Score 15; DB 8; Length 164921;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 60
AC009346/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

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AC009346 168448 bp DNA linear INV 22-FEB-2001
 Drosophila melanogaster, chromosome 3R, region 83A-83B, BAC clone
 BACR03P13, complete sequence.
 AC009346
 AC009346.5 GI:13096029
 HTG.
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 168448)
 Ceiniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H.,
 Holt, R.A., Evans, C.A., Gocayne, J.D., Amaratunga, P.G., Brandon, R.C.,
 Rogers, Y., An, H., Baldwin, D., Barzon, J., Beeson, K.Y., Busam, D.A.,
 Carlson, J.W., Center, A., Champagne, M., Davenport, L.B., Dietz, S.M.,
 Dodson, K., Dorsett, V., Doup, L.E., Doyle, C., Dresnek, D., Fartan, D.,
 Ferreira, S., Frisoe, E., Galle, R.F., Garg, N.S., George, R.A.,
 Gonzalez, M., Houch, J., Hoskins, R.A., Hostin, D., Howland, T.J.,
 Ibegwam, C., Jalali, M., Kruse, D., Li, P., Mattei, B., Moshrefi, A.,
 McIntosh, T.C., Moy, M., Murphy, B., Nelson, C., Nelson, K.A., Nunco, J.,
 Pacled, J., Paragas, V., Park, S., Patel, S., Pfeiffer, B.,
 Phouanavong, S., Piltman, G.S., Puri, V., Richards, S., Scheeler, F.,
 Stapleton, M., Strong, R., Svitek, R., Tector, C., Williams, S.M.,
 Zaveri, J.S., Smith, H.O., Rubin, G.M., and Venter, J.C.
 Sequencing of Drosophila chromosome 3R, region 83A-83B
 Unpublished
 2 (bases 1 to 168448)
 Ceiniker, S.E., Agbayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G.,
 Butenoff, C., Champagne, M., Chavez, C., Chew, M., Ciesiolka, L.,
 Doyle, C.M., Fartan, D.B., Galle, R., George, R.A., Harris, N.L.,
 Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L.,
 Kim, E., Lee, B., Lewis, S., Li, P., Lomota, M.A., Marda, P.,
 Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacled, J., Pfeiffer, B.,
 Pfeiffer, B., Poon, L., Sequiera, A., Sethi, H., Shit, E.,
 Svitek, R.R., Wan, K.H., Weinburg, T., Zhang, R., Zieran, L.L. and
 Rubin, G.M.
 Direct Submission
 Submitted (17-AUG-1999) Drosophila Genome Center, Lawrence Berkeley
 Laboratory, MS 64-121, Berkeley, CA 94720, USA
 On Feb 22, 2001 this sequence version replaced gi:7143384.
 Sequence submitted by:
 Berkeley Drosophila Genome Project
 Lawrence Berkeley National Laboratory, MS 64-121
 Berkeley, CA 94720
 This sequence was assembled using end sequences from a whole genome
 shotgun and from subclones of this BAC and its neighboring clones.
 For further information about this sequence, including its location
 and relationship to other sequences, please visit our sequence
 archive Web site (<http://www.fruitfly.org/sequence/>) or send email
 to bdgp@fruitfly.berkeley.edu.
 Location/Qualifiers
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 /organism="Drosophila melanogaster"
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 /clone="BACR03P13 (D672)"
 /clone_11b="RPCI-98 (Roswell) Park Cancer Institute
 Drosophila melanogaster BAC library, partial EcoRI in
 pBACE3.6")
 ORIGIN
 BASE COUNT 46234 a 37731 c 38029 g 46454 t
 Query Match. 71.4%; Score 15; DB 3; Length 168448;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCTCAACGTTGCA 15
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Db 59973 TCCTCAACGTTGCA 59959

RESULT 61
SC0939126

LOCUS
DEFINITION
ACCESSION
AL035212 AL035478 AL049727 AL132824 AL132997 AL589708 AL591522
AL645882
AL939126.1 GI:24413894

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

1 Streptomyces coelicolor A3(2)
Streptomyces coelicolor A3(2)
Bacteria; Actinobacteriae; Actinomycetales;
Streptomycinae; Streptomycetaceae; Streptomyces.

1 Bentley, S.D., Chater, K.F., Cerdeno-Tarraga, A.M., Challis, G.L.,
Thomson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kiese, H.,
Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M.,
Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S.,
Huang, C.H., Kiese, T., Larke, L., Murphy, L., Oliver, K., O'Neill, S.,
Rabinowitsch, E., Rajandream, M.A., Rutherford, K., Rutter, S.,
Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S.,
Taylor, K., Warren, T., Wietzorek, A., Woodward, V., Barrell, B.G.,
Partridge, L., and Hopwood, D.A.
Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)
Nature 417 (6885), 141-147 (2002)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

2 Bentley, S.D.
21996410
12000953
2 (bases 1 to 295150)

Direct Submission
Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces
sequencing team, Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: sds@sanger.ac.uk
On or before Oct 26, 2002 this sequence version replaced
gi:20520744, gi:20520662, gi:20520663, gi:20520667, gi:20520669,
gi:20520764, gi:20520816, gi:20520670, gi:20520820, gi:20520846,
gi:20520823, gi:20520863, gi:20520869.

FEATURES
source
RBS
gene
CDS

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/strain="A3(2)"
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524..1933
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/note="SC7B7.02, possible lipoprotein, len: 469; has
similarity to signal sequence of Mycobacterium lepre
hypothetical protein TR:E334742 (EMBL:298604) MLCB2052.27
(445 aa), fasta scores: opt: 75 z-score: 199.2 E():
0.00062, 23.3% identity in 335 aa overlap. Contains
N-terminal signal sequence and appropriately positioned
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site"
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misc_feature
gene
CDS

1941..3002
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/note="synonym: SC7B7.03"
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protein, len: 353 aa; similar to many members of the MALFG
subfamily of the binding-protein-dependant transport
system membrane proteins eg. MSMP_STRMU_Q00750 multiple
sugar-binding transport system permease protein (290 aa),
fasta scores: opt: 393 z-score: 636.8 E(): 2.6e-28, 32.5%
identity in 280 aa overlap. Contains PS00402
Binding-protein-dependent transport systems inner membrane
comp signature"
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/db_xref="GI:2661678"
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/note="SCO6007, probable integral membrane transport
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systems membrane proteins eg. TR:Q06111 (EMBL:X66092)
putative transport system permease protein from
Clostridium perfringens (275 aa), fasta scores: opt: 590
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/note="synonym: SC7B7.05"
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5462..5466
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5475..6590
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5475..6590
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/note="SC7B7.06, probable solute-binding protein of transmembrane transport system, len: 403 aa; similar to many eg. XYLX ECOLI P37387 d-xylose-binding periplasmic protein precursor (330 aa), fasta scores: opt: 619 z-score: 573.4 E(): 8.9e-25, 35.7% identity in 325 aa overlap. Contains N-terminal signal sequence and appropriately positioned P800013 Prokaryotic membrane lipoprotein lipid attachment site"
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Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 17025 TCGTCGACGTTGCA 17039

RESULT 62

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DIPOSOPIHILA melanogaster chromosome 3R, section 6 of 118 of the complete sequence.
ACCESSION AE003602 AE014297
VERSION AE003602.3 GI:23170357
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

AE003602 296091 bp DNA linear INV 14-FEB-2003
DIPOSOPIHILA melanogaster chromosome 3R, section 6 of 118 of the complete sequence.
ACCESSION AE003602 AE014297
VERSION AE003602.3 GI:23170357
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

DIPOSOPIHILA melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 296091)
Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F., George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N., Sutton,G.G., Wortman,J.R., Yeandle,M.D., Zhang,Q., Chen,L.X., Brandon,R.C., Rogers,Y.H., Blazer,V.G., Champs,M., Pfeiffer,B.D., Wan,K.H., Doyle,C., Baxter,E.G., Helt,G., Nelson,C.R., Gaber,G.L., Abtill,J.F., Agbayani,A., An,H.J., Andrews-Pfannkoch,C., Balwin,D., Ballew,R.M., Baau,A., Baxendale,J., Bayraktaroglu,L., Beasley,E.M., Beeson,K.Y., Benos,P.V., Berman,B.P., Bhandari,D., Bolshakov,S., Borkova,D., Botchan,M.R., Bouck,J., Brodeur,P., Brothier,P., Butte,K.C., Buam,D.A., Butler,H., Cadenot,E., Center,A., Chandra,I., Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de Pablos,B., Delcher,A., Deng,Z., May,A.D., Dew,I., Dietz,S.M., Dodson,K., Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Fieriera,S., Fleischmann,W., Foster,C., Gabrielian,A.E., Gary,N.S., Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z., Guan,P., Harris,M., Hartig,N.L., Harvey,D., Heiman,T.J., Hernandez,J.R., Houck,J., Hoeltlin,D., Houston,K.A., Howland,T.J., Wei,M.H., Ibegwam,C., Jalili,M., Kalush,F., Karpen,G.H., Ke,Z., Kemison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C., Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A., Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Matei,J., McIntosh,T.C., McLeod,M.P., McPherson,D., Mekulov,G., Milshina,N.V., Mobarry,C., Morris,J., Mosher,B., Mount,S.M., Moy,M., Murphy,B., Murphy,L., Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K., Nuskern,D.R., Pacile,D.M., Palazolo,M., Pittman,G.S., Pan,S., Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K., Sanders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siders-Kiamos,I., Simpson,M., Skupski,M.P., Smith,T., Spter,E., Spradling,A.C., Stempleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wasserman,D.A., Weinstein,G.M., Weisenbach,J., Williams,S.M., Woodaet, Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yen,R.P., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
Science 287 (5461), 2185-2195 (2000)
20196006
10731132
2 (bases 1 to 296091)
Celniker,S.E., Adams,M.D., Kronmiller,B., Wan,K.H., Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C., Rogers,Y., Banzon,J.J., An,H., Baldwin,D., Banzon,K.Y., Bausam,D.A., Carlson,J.W., Center,A., Champs,M., Davenport,L.B., Dietz,S.M., Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Fartan,D., Ferriera,S., Frise,E., Galle,R.F., Gary,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalili,M., Kruse,D., Li,P., Mattei,B., Mosher,B., Beeson,K.Y., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J., Pacile,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stempleton,M., Strong,R., Svirskas,R., Tector,C., Tyler,D., Williams,S.M., Zaveri,J.S., Smith,H.O., Venter,J.C. and Rubin,G.M.
Sequencing of Drosophila melanogaster genome
Unpublished
3 (bases 1 to 296091)
Mitra,S., Crosby,M.A., Matthews,B.B., Bayraktaroglu,L., Campbell,K., Hradecky,P., Huang,Y., Kaminker,J.S., Prochownik,S.E.,

JOURNAL	TITLE
AUTHORS	Smith C.D., Tupry J.L., Bergman,C.M., Betman,B.P., Carlson,J.W., Celinker,S.E., Clamp,M.E., Drysdale,R.A., Emmert,D., Frisbe,E., de Grey,A.D.N.J., Harris,N.L., Krommiller,B., Marchall,B., Milburn,G.H., Richter,J., Russo,S., Searle,S.M.J., Smith,E., Shu,S., Smutniak,F., Whitfield,E.J., Ashburner,M., Gelbart,W.M., Rubin,G.M., Mungall,C.J. and Lewis,S.E.
JOURNAL	Annotation of Drosophila melanogaster genome
AUTHORS	Unpublished
CONSRM	4 (bases 1 to 296091)
JOURNAL	Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850 USA
AUTHORS	5 (bases 1 to 296091)
CONSRM	FlyBase
JOURNAL	Direct Submission
AUTHORS	Submitted (06-SEP-2002) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA
REMARK	6 (bases 1 to 296091)
FEATURES	· FlyBase Direct Submission Submitted (13-FEB-2003) University of California Berkeley, 539 Life Sciences Addition, Berkeley, CA 94720, USA Sequence update by submitter On Sep 18, 2002 this sequence version replaced gi:10727155. Location/Qualifiers 1..296091 /organism="Drosophila melanogaster" /mol_type="genomic DNA" /db_xref="taxon:7227" /chromosome="3R" /note="genotype: Y[1]; cn[1] bw[1] ep[1]; Rh6[1]" complement(2617..3157) /locus_tag="TE20308" /map="83A3-83A3" complement(2617..3157) /transposon="G4{} 1220" /db_xref="FLYBASE:FBc10020308" 5404..11806 /locus_tag="TE19305" /map="83A3-83A3" 5404..11806 /transposon="Burdock{} 1221" /db_xref="FLYBASE:FBc10019305" 13991..15004 /locus_tag="CG14669" /note="Last curated on Sat Mar 23 16:32:50 PST 2002"
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CDS
Query Match      10.4%; Score 15; DB 3; Length 296091;
Best Local Similarity 70.0%; Pred. No. 1,1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 TCGTCGAAGCTTCCA 15
|||||
|||||
|||||
|||||
|||||
Db      190044 TCGTCGAAGCTTCCA 190030

RESULT 63
AP005958/c      302650 bp      DNA      linear      BCT 28-MAR-2003
LOCUS      Bradyrhizobium japonicum USDA 110 DNA, complete genome, section
DEFINITION      24/31.
ACCESSION      AP005958 BA000040
VERSION      AP005958.1 GI:27354550
KEYWORDS

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/transl_table=11
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/protein_id="BAC51543.1"
/db_xref="GI:27354557"
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GARAFEGVMDLRHCAVNOAVNFGKPVVDLDTWGLVREGIARPPVAEYIRP
MYAPNGIGGGVLPETTDWCLCIYESPIPEVGSATITLSPFRRTACAPADYKAS
CLYPSRSLREASRGFONCLMDMLNTEFGSNVEMAKDGVFTPADNGTFLNG
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YARAKLYWDFAHKMKLAA"
gene complement (8909. .9784)
/gene="b116279"
CDS complement (8909. .9784)
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/note="ORF ID: b116279"
hypothetical protein
/codon_start=1
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/protein_id="BAC51544.1"
/db_xref="GI:27354558"
/translation="MRVTRMRCREIGIADDAADLTTRGPRSRDVIIDGLRLS
VRETDSPFRFGYMLHNDAPVGLQILHTANDGSGSIRCNLSKVEPAFRTYAP
MLTKVAQHKQDVTYVNIISPAEWTVQVIGQGRRCYCGILFSPALSPARAVEV
RODAQIDGLSEADVLLARHAYGCLCLICASDGRAPFVLQPMRVRRLMLMOM
IYCPVDVYVVCAGIIGRFLLRRGISIALDANGPVGLVIGYREPIGRKTKGPHCP
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gene complement (9781. .10938)
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CDS complement (9781. .10938)
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/codon_start=1
/transl_table=11
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/db_xref="GI:27354559"
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SDAALMSTEROLFLLAAAGLCVRLHPTMEATPSEMGDRVRYRIGDILNN
RLDGIYVGAERPAASLDEPRTTFAIADMARNTTSSVPSCLAYGATLHDGVT
RHKPTKCFGVFAQKTRHHPMDVPTFRIPPARMNEVEEDLSDGYSVLTSAB
AGVDCFVQOQNSLFVHFCQGEYETOSLIGLRDMGRFLGENEVCPTIPRGYLNK
GAEIILAFRQKALSDROPFLPADFPADQLTRDLNVMHLPAQHTYRMMLQVMSQPA

Query Match 71.4%; Score 15; DB 1; Length 302650;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 CGTCGACGCTTCG 16
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Db 132468 CGTCGACGCTTCG 132454

RESULT 64
AX592408 14 bp DNA linear PAT 27-JAN-2003
LOCUS Sequence 98 from Patent WO02052002.
ACCESSION AX592408
VERSION AX592408.1 GI:27950510
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon, K.L. and Dina, D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 98 04-JUL-2002;
Dynavax Technologies Corporation (US)

FEATURES
source Location/Qualifiers
1. .14
/organism="synthetic construct"
/mol_type="genomic DNA"
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/note="Polynucleotide containing CG"
BASE COUNT 2 a 4 c 4 g 4 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCTCGAACGTTTCG 14
|||||
Db 1 TCCTCGAACGTTTCG 14

RESULT 65
AX592321 16 bp DNA linear PAT 27-JAN-2003
LOCUS Sequence 11 from Patent WO02052002.
ACCESSION AX592321
VERSION AX592321.1 GI:27950423
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon, K.L. and Dina, D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 11 04-JUL-2002;
Dynavax Technologies Corporation (US)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:32630"
/note="Polynucleotide containing CG"
BASE COUNT 2 a 4 c 4 g 6 t
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 16;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCCTCGAACGTTTCG 14
|||||
Db 1 TCCTCGAACGTTTCG 14

RESULT 66
AX592339 18 bp DNA linear PAT 27-JAN-2003
LOCUS Sequence 29 from Patent WO02052002.
ACCESSION AX592339
VERSION AX592339.1 GI:27950441
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon, K.L. and Dina, D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 29 04-JUL-2002;
Dynavax Technologies Corporation (US)
FEATURES
source Location/Qualifiers
1. .18
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

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BASE COUNT 4 a /note="n = 5-bromocytosine" 1 others
ORIGIN 3 c 5 g 5 t

Query Match 66.7%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19
|||||
Db 5 GAACGTCGAGATG 18

RESULT 67
AX592354 18 bp DNA linear PAT 27-JAN-2003
LOCUS AX592354
DEFINITION Sequence 44 from Patent WO02052002.
ACCESSION AX592354
VERSION AX592354.1 GI:27950456
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 44 04-JUL-2002;
DynaVax Technologies Corporation (US)
location/Qualifiers

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/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 4 a 3 c 6 g 5 t
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19
|||||
Db 5 GAACGTCGAGATG 18

RESULT 68
AX592333 19 bp DNA linear PAT 27-JAN-2003
LOCUS AX592333
DEFINITION Sequence 23 from Patent WO02052002.
ACCESSION AX592333
VERSION AX592333.1 GI:27950435
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 23 04-JUL-2002;
DynaVax Technologies Corporation (US)
location/Qualifiers

FEATURES
source 1.19
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/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

misc_feature 2
/note="n = 5-bromocytosine"

misc_feature 5
/note="n = 5-bromocytosine"

BASE COUNT 4 a 2 c 6 g 5 t 2 others
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19
|||||
Db 6 GAACGTCGAGATG 19

RESULT 69
AX592334 19 bp DNA linear PAT 27-JAN-2003
LOCUS AX592334
DEFINITION Sequence 24 from Patent WO02052002.
ACCESSION AX592334
VERSION AX592334.1 GI:27950436
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 24 04-JUL-2002;
DynaVax Technologies Corporation (US)
location/Qualifiers

FEATURES
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

misc_feature 5
/note="n = 5-bromocytosine"

BASE COUNT 4 a 3 c 6 g 5 t 1 others
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATG 19
|||||
Db 6 GAACGTCGAGATG 19

RESULT 70
AX592365 20 bp DNA linear PAT 27-JAN-2003
LOCUS AX592365
DEFINITION Sequence 55 from Patent WO02052002.
ACCESSION AX592365
VERSION AX592365.1 GI:27950467
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Fearon,K.L. and Dina,D.
TITLE Immunomodulatory polynucleotides and methods of using the same
JOURNAL Patent: WO 02052002-A 55 04-JUL-2002;
DynaVax Technologies Corporation (US)
location/Qualifiers

FEATURES
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/note="Polynucleotide containing CG"

BASE COUNT 4 a 4 c 7 g 5 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 7 GAACGTCGAGATG 20

RESULT 71
AX174913 22 bp DNA linear PAT 03-JUL-2001
LOCUS AX174913
DEFINITION Sequence 1 from Patent WO0143778.
ACCESSION AX174913
VERSION AX174913.1 GI:14598409
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 Felgner, P.L. and Zepf, H. O.
AUTHORS Use of cationic lipids for intracellular protein delivery
TITLE Patent: WO 0143778-A 1 21-JUN-2001;
JOURNAL Gene Therapy Systems, Inc. (US)
FEATURES
source location/Qualifiers
1..24
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Synthetic peptide"
modified_base 1
/note="n=T-NH2"
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modified_base 22
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/mod_base=OTHER

BASE COUNT 5 a 7 g 5 t 2 others
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATG 19
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Db 8 GAACGTCGAGATG 21

RESULT 72
AX252517 24 bp DNA linear PAT 05-OCT-2001
LOCUS AX252517
DEFINITION Sequence 9 from Patent WO0168103.
ACCESSION AX252517
VERSION AX252517.1 GI:15985788
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 van Nee, G.
AUTHORS Methods of ameliorating symptoms of herpes infection using
TITLE immunomodulatory polynucleotide sequences
JOURNAL Patent: WO 0168103-A 9 20-SEP-2001;
Dynamax Technologies Corporation (US)
FEATURES
source location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 4 a 6 c 6 g 8 t
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTG 14
|||||
Db 1 TCGTGAACGTTG 14

RESULT 73
AX253133 24 bp DNA linear PAT 05-OCT-2001
LOCUS AX253133
DEFINITION Sequence 11 from Patent WO0168077.
ACCESSION AX253133
VERSION AX253133.1 GI:15986301
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 van Nee, G.
AUTHORS Methods of preventing and treating viral infections using
TITLE immunomodulatory polynucleotide sequences
JOURNAL Patent: WO 0168077-A 11 20-SEP-2001;
Dynamax Technologies Corporation (US)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 4 a 6 c 6 g 8 t
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTG 14
|||||
Db 1 TCGTGAACGTTG 14

RESULT 74
AX592311 24 bp DNA linear PAT 27-JAN-2003
LOCUS AX592311
DEFINITION Sequence 1 from Patent WO02052002.
ACCESSION AX592311
VERSION AX592311.1 GI:27950413
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 Fearon, K.L. and Dina, D.
AUTHORS Immunomodulatory polynucleotides and methods of using the same
TITLE Patent: WO 02052002-A 1 04-JUL-2002;
JOURNAL Dynamax Technologies Corporation (US)
FEATURES
source location/Qualifiers
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
/note="Polynucleotide containing CG"

BASE COUNT 4 a 6 c 6 g 8 t
ORIGIN

Query Match 66.7%; Score 14; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTG 14
|||||
Db 1 TCGTGAACGTTG 14

RESULT 75

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2003, 09:15:24 / Search time 1313 Seconds
(without alignments)
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Title: US-10-033-243-132

Perfect score: 21

Sequence: 1 tcgtcgaacttcgagatgatc 21

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 22781392 seqs, 12152238056 residues

Word size: 0

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database:

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2: em_esthum:*
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4: em_estov:*
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12: gb_est3:*
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14: gb_est5:*
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16: em_estom:*
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18: em_ges_inv:*
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20: em_ges_vrt:*
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22: em_ges_mam:*
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25: em_ges_rtd:*
26: em_ges_phg:*
27: em_ges_vrt1:*
28: gb_ges1:*
29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	ID	Description
C 1	15	71.4	194	13	BU095678	BU095678 tca-163 t
C 2	15	71.4	337	12	BI511039	BI511039
C 3	15	71.4	390	9	AI945022	AI945022 b08b02.y
C 4	15	71.4	432	12	BI510669	BI510669 BB160003A

5	15	71.4	609	28	AQ623639	AQ623639 HS_5377_A
6	15	71.4	728	28	BH816458	BH816458 AM_Ba002
7	15	71.4	842	29	BZ391656	BZ391656 EINCQ64TR
8	15	71.4	889	14	CD375545	CD375545 PTMM00709
9	15	71.4	913	13	BK455352	BK455352 BK455352
10	15	71.4	1220	29	CC235774	CC235774 CH261-139
11	14	66.7	108	11	CNS09N54	BK066068 Single re
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14	14	66.7	348	11	CNS09O90	BK070096 Single re
15	14	66.7	387	12	BI507844	BI507844 BB170008B
16	14	66.7	414	12	BI505056	BI505056 BB170012B
17	14	66.7	424	14	CB333691	CB333691 T9ESTzyf6
18	14	66.7	433	12	BM629296	BM629296 170006874
19	14	66.7	439	28	AQ252378	AQ252378 HS_2262_A
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21	14	66.7	469	11	CNS09GNZ	BK057675 Single re
22	14	66.7	484	9	AA097939	AA097939 mt82501.r
23	14	66.7	486	12	BM636144	BM636144 170006875
24	14	66.7	492	12	BM652631	BM652631 170006873
25	14	66.7	493	12	BM644091	BM644091 170006874
26	14	66.7	499	12	BM597612	BM597612 170006874
27	14	66.7	504	12	BM611518	BM611518 170006871
28	14	66.7	512	12	BM866297	BM866297 mgc8005XB
29	14	66.7	513	14	CB358730	CB358730 ZF001-P00
30	14	66.7	521	28	BH899325	BH899325 Oc600392
31	14	66.7	527	12	BM618536	BM618536 170006874
32	14	66.7	528	12	BM618261	BM618261 170006874
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34	14	66.7	528	29	TA99D10P	TA99D10P T.Bruecl
35	14	66.7	533	12	BM641866	BM641866 170006873
36	14	66.7	534	28	AQ407920	AQ407920 HS_5055_B
37	14	66.7	541	9	AL654922	AL654922 AL654922
38	14	66.7	544	12	BI511012	BI511012 BB160004A
39	14	66.7	546	12	BM649585	BM649585 170006873
40	14	66.7	549	12	BM650226	BM650226 170006873
41	14	66.7	550	12	BM626834	BM626834 170006874
42	14	66.7	554	12	BM633500	BM633500 170006875
43	14	66.7	556	28	BH899413	BH899413 Oc600480
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45	14	66.7	561	12	BM632387	BM632387 170006875
46	14	66.7	562	12	BM600003	BM600003 170006870
47	14	66.7	569	12	BM621639	BM621639 170006874
48	14	66.7	571	12	BM619639	BM619639 170006874
49	14	66.7	572	12	BM645614	BM645614 170006873
50	14	66.7	578	9	AL667035	AL667035 Ec24912.Y
51	14	66.7	578	12	BM650798	BM650798 170006873
52	14	66.7	582	12	BM279238	BM279238 NB.ad1.04
53	14	66.7	583	10	BF157792	BF157792 E14905.Y
54	14	66.7	588	12	BM630963	BM630963 170006875
55	14	66.7	592	12	BM649878	BM649878 170006873
56	14	66.7	593	12	BM624679	BM624679 170006874
57	14	66.7	595	12	BM622534	BM622534 170006874
58	14	66.7	595	12	BM632552	BM632552 170006875
59	14	66.7	600	12	BM639133	BM639133 170006875
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61	14	66.7	606	12	BM621612	BM621612 170006874
62	14	66.7	606	28	BH416973	BH416973 1007052A0
63	14	66.7	614	12	BM634523	BM634523 170006875
64	14	66.7	616	12	BM625508	BM625508 170006874
65	14	66.7	617	28	AQ880074	AQ880074 HS_4867.A
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67	14	66.7	627	29	CC120030	CC120030 ND.L.76020
68	14	66.7	628	9	AM288450	AM288450 M8TMDA19
69	14	66.7	628	12	BM641079	BM641079 170006873
70	14	66.7	629	12	BM622163	BM622163 170006874
71	14	66.7	629	12	BM655453	BM655453 170006873
72	14	66.7	631	12	BM625565	BM625565 170006874
73	14	66.7	631	12	BM654222	BM654222 170006873
74	14	66.7	636	12	BM597192	BM597192 170006874
75	14	66.7	636	12	BM636272	BM636272 170006879
76	14	66.7	637	12	BM639355	BM639355 170006875
77	14	66.7	640	9	AL697586	AL697586 AL697586

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
C 78	14 66.7	640 12	BM628043							
C 79	14 66.7	645 12	BM620206							
C 80	14 66.7	655 12	BM600219							
C 81	14 66.7	656 12	BM591083							
C 82	14 66.7	658 12	BM650161							
C 83	14 66.7	659 12	BM646108							
C 84	14 66.7	660 12	BM646396							
C 85	14 66.7	660 12	BM655738							
C 86	14 66.7	662 12	BM585671							
C 87	14 66.7	662 12	BM634377							
C 88	14 66.7	662 12	BM635562							
C 89	14 66.7	666 12	BM577468							
C 90	14 66.7	667 12	BM623340							
C 91	14 66.7	670 12	BM639444							
C 92	14 66.7	671 12	BM619604							
C 93	14 66.7	672 12	BM638432							
C 94	14 66.7	672 12	BM655524							
C 95	14 66.7	673 12	BM619765							
C 96	14 66.7	677 12	BM636942							
C 97	14 66.7	680 12	BM623418							
C 98	14 66.7	681 13	BX468200							
C 99	14 66.7	683 12	BM624318							
C 100	14 66.7	684 12	BM622788							

ALIGNMENTS

RESULT 1
BU095678 194 bp mRNA linear EST 14-MAR-2003
tca-163 tca Trypanosoma carassii cDNA clone 01n14 5', mRNA
sequence.
BU095678
ACCESSION BU095678.1 GI:25123402
EST.
KEYWORDS Trypanosoma carassii
ORGANISM Trypanosoma carassii
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.

REFERENCE 1 (bases 1 to 194)
Aguero, F., Campo, V., Cremenon, L., Jager, A., Di Noia, J.M., Overath, P., Sanchez, D.O. and Frasch, A.C.
Gene discovery in the freshwater fish parasite Trypanosoma carassii: identification of trans-sialidase-like and mucin-like genes
Infect. Immun. 70 (12), 7140-7144 (2002)
CONTACT: Sanchez DO
Genomics and Bioinformatics
Instituto de Investigaciones Biologicas
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos Aires, Argentina
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@ib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with crossmatch (see http://www.phrap.org). Sequences were then trimmed from both ends to remove low quality bases and masked vector.
Plate: 01 row: n column: 14
Seq primer: T7
Location/Qualifiers

FEATURES

1..194
/organism="Trypanosoma carassii"
/mol_type="mRNA"
/db_xref="taxon:38249"
/clone="01n14"
/dev_stage="blood trypanastigote"
/lab_host="Goldfish (Carassius auratus)"
/clone_lib="tca"
/note="vector: pSport1; Blood trypanastigotes were obtained from goldfish and cultured as described (Overath et al. Parasitol Res (1998) 84:343) before obtaining total RNA using TRIzol. cDNA library construction was made from

polyA+ mRNA using a poly-dT oligonucleotide as primer. The cDNAs were cloned in a oriented manner using a commercial kit (Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning, Life Technologies)."

Query Match 71.4%; Score 15; DB 13; Length 194;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ORIGIN 60 a 35 c 40 g 59 t
1 TCGTGAACGTTCCA 15
Db 149 TCGTGAACGTTCCA 135

RESULT 2
B1511039/c 337 bp mRNA linear EST 08-APR-2002
B1511039
LOCUS B1511039.1 B160004A20G12.5 Bee Brain Normalized Library, B1516 Apis mellifera
DEFINITION cDNA clone B160004A20G12 5', mRNA sequence.
B1511039
ACCESSION B1511039.1 GI:15361413
EST.
KEYWORDS Apis mellifera (honeybee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.

REFERENCE 1 (bases 1 to 337)
Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L., Pardini, J., Robertson, H.M., Soares, B. and Robinson, G.E.
Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee
Genome Res. 12 (4), 555-566 (2002)
21929762
JOURNAL MEDLINE
COMMENT

CONTACT: Gene E. Robinson
Department of Entomology
University of Illinois
505 S. Goodwin Ave., Urbana, IL 61801, USA
Tel: 217 265 0309
Fax: 217 244 3499
Email: gene@life.uiuc.edu
This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
PCR Primers
FORWARD: TAATACGACTCCTATAGG
BACKWARD: ATTACCCCTCCTAAG
Plate: B160004A20 row: G column: 12
Seq primer: AGCGATACCAATTTCACACGA
High quality sequence stop: 337.
Location/Qualifiers

FEATURES

1..337
/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly A.m. ligustica"
/db_xref="taxon:7460"
/clone="B160004A20G12"
/sex="female"
/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DHI0B"
/clone_lib="Bee Brain Normalized Library, B1516"
/note="Organ: brain; Vector: pTR3-Pac; Site 1: ECOR1; Site 2: Notcl; The B1516 library was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806. RNA was prepared from dissected brains of adult worker bees of

BASE COUNT 123 a 59 c 64 g 91 t
 ORIGIN various ages and various behavioral groups."

Query Match 71.4%; Score 15; DB 12; Length 337;
 Best Local Similarity 100.0%; Pred. No. 78;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTGAACGTTTGA 15
 |||||
 |||||
 Db 264 TCGTGAACGTTTGA 250

RESULT 3
 A1945022/c 390 bp mRNA linear EST 08-JAN-2001

LOCUS b808b02.y1 Drosophila melanogaster adult testis library Drosophila
 DEFINITION melanogaster cDNA clone b808b02 5', mRNA sequence.

ACCESSION A1945022
 VERSION A1945022.2 GI:9990370
 KEYWORDS EST.
 SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.

REFERENCE 1 (bases 1 to 390)
 Andrews, J., Bouffard, G.G., Cheadle, C., Lu, J., Becker, K.G. and
 Oliver, B.

TITLE Gene discovery using computational and microarray analysis of
 transcription in the drosophila melanogaster testis

JOURNAL Genome Res. 10 (12), 2030-2043 (2000)
 MEDLINE 20568492
 PUBMED 1116097

COMMENT On Aug 17, 1999 this sequence version replaced gi:5735420.
 Contact: Brian Oliver
 Laboratory of Cellular and Developmental Biology
 NIDDK, National Institutes of Health
 6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
 Fax: (301) 496 5239

Email: oliverb@helix.nih.gov,
 http://www.nidk.nih.gov/intram/people/boliver.htm
 Tissue isolation and library construction performed at the National
 Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
 http://www.nidk.nih.gov/intram/people/boliver.htm). DNA sequencing
 and analyses performed by National Institutes of Health Intramural
 Sequencing Center (NISC; see http://www.nisc.nih.gov).

Plate: 08 row: b column: 02
 Seq primer: M33RP1 reverse primer (ABT).

FEATURES
 Location/Qualifiers
 1..390

source
 /organism="Drosophila melanogaster"
 /mol_type="mRNA"

/strain="Y[*] w[67c1]/Y"
 /db_xref="taxon:7227"

/clone="b808b02"
 /sex="male"

/dev_stage="1-5 day adult"
 /lab_host="SOLR (Stratagene)"

/clone_lib="Drosophila melanogaster adult testis library"
 /note="Organ: testis; Vector: pBluescript SK (Stratagene);
 Site_1: EcoR I; Site_2: Xho I; Testes dissected from 1-5
 day adult Y[*] w[67c1]/Y males raised at 25°C. RNA
 isolated using Trizol (Life Technologies) and a single
 round of Poly(A)+ selection using Oligotex (Qiagen). cDNA
 library constructed using Stratagene Zap-cDNA synthesis
 kit. Oligo dT-primed, size fractionated -1-6 kb and
 directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
 Following a single round of amplification pBluescript SK
 phagemids were mass excised. A distribution channel for
 clones is being sought, but not currently available.
 Requests for clones cannot be honored."

BASE COUNT 121 a 77 c 109 g 83 t

ORIGIN

Query Match 71.4%; Score 15; DB 9; Length 390;
 Best Local Similarity 100.0%; Pred. No. 79;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTGAACGTTTGA 15
 |||||
 |||||
 Db 94 TCGTGAACGTTTGA 80

RESULT 4
 B1510669/c 432 bp. mRNA linear EST 08-APR-2002

LOCUS B160003A20G01.5 Bee Brain Normalized library, B16 Apis mellifera
 DEFINITION cDNA clone B160003A20G01 5', mRNA sequence.

ACCESSION B1510669
 VERSION B1510669.1 GI:15361043
 KEYWORDS EST.
 SOURCE Apis mellifera (honeybee)

ORGANISM Apis mellifera
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
 Apidae; Apis.

REFERENCE 1 (bases 1 to 432)
 Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
 Pardinas, U., Robertson, H.M., Soares, B. and Robinson, G.E.
 Annotated expressed sequence tags and cDNA microarrays for studies
 of brain and behavior in the honey bee

JOURNAL Genome Res. 12 (4), 555-566 (2002)
 MEDLINE 21929762
 PUBMED 11932240

COMMENT Contact: Gene E. Robinson
 Department of Entomology
 University of Illinois
 505 S. Goodwin Ave., Urbana, IL 61801, USA
 Tel: 217 265 0309
 Fax: 217 244 3499

Email: gene@life.uiuc.edu
 This research was funded by the University of Illinois Critical
 Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
 Award in Functional Genomics to G.E. Robinson and an NSF
 Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.

PCR Primers
 FORWARD: TAATCGACTCACTATAGCG
 BACKWARD: ATTACCTCCTCAAG
 Plate: B160003A20 row: G column: 01
 Seq primer: AGCGATTAACAATTCAACACAGA

High quality sequence stop: 432.

FEATURES
 Location/Qualifiers
 1..432

source
 /organism="Apis mellifera"
 /mol_type="mRNA"

/strain="mixed strains of European bees, predominantly
 A.m. ligustica"

/db_xref="taxon:7460"
 /clone="B160003A20G01"

/sex="female"

/tissue_type="brain"
 /dev_stage="adult worker honey bee"

/lab_host="DH10B"

/clone_lib="Bee Brain Normalized library, B16"
 /note="Organ: brain; Vector: pTRT3-Pac; Site_1: EcoRI;
 Site_2: NotI; The B16 library was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996). Genome Research 6(9): 791-806. RNA was
 prepared from dissected brains of adult worker bees of
 various ages and various behavioral groups."

BASE COUNT 163 a 69 c 102 g 98 t

Query Match 71.4%; Score 15; DB 12; Length 432;

Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTGCA 15
|||||
Db 58 TCGTCGAACGTTGCA 44

RESULT 5
AO623639 609 bp DNA linear GSS 16-JUN-1999
LOCUS
DEFINITION HS_5377_A2_F05_S06E_RPCT-11 Human Male BAC Library Homo sapiens
genomic clone Plate=953 Col=10 Row=K, genomic survey sequence.

ACCESSION AO623639
VERSION AO623639.1 GI:5086119
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 609)
Mahairas,G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

JOURNAL
MEDLINE
PubMed
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCT-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACpac Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Research Genetics (info@resgen.com). BAC end web server:
http://www.htsc.washington.edu
Plate: 953 row: K column: 10
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 609.

FEATURES
source
1.609
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=953 Col=10 Row=K"
/sex="male"
/clone_lib="RPCT-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

BASE COUNT 185 a 124 c 162 g 125 t 13 others

Query Match 71.4%; Score 15; DB 28; Length 609;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTGCA 15
|||||
Db 335 TCGTCGAACGTTGCA 349

RESULT 6
BH816458

LOCUS BH816458 728 bp DNA linear GSS 08-MAY-2002
DEFINITION AM_BA002JU24f Apis mellifera Apis mellifera genomic clone
AM_BA002JU24f, genomic survey sequence.

ACCESSION BH816458
VERSION BH816458.1 GI:20512115
KEYWORDS GSS.
SOURCE Apis mellifera (honeybee)
ORGANISM Apis mellifera
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
Apidae; Apis.

REFERENCE 1 (bases 1 to 728)
Tomkins,J.P., Luo,M., Hunt,G., Main,D., Friesch,D., Page,P.E.,
Guzman-Nova,E. and Wing,R.A.

TITLE Development of Genomic Resources for honey bee (Apis mellifera L.):
BAC Library Construction, Preliminary STC Analysis, and
Identification of Clones Associated With Behavioral Traits
Unpublished
Contact: Tomkins JP
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson University, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: jtomkins@clemson.edu
Total hg bases = 231
Seq primer: TAATACGACTCACTATAGG
Class: BAC ends
High quality sequence start: 52
High quality sequence stop: 502.

FEATURES
source
1.728
Location/Qualifiers
/organism="Apis mellifera"
/mol_type="genomic DNA"
/strain="Africanized honey bee"
/db_xref="taxon:7460"
/clone="AM_BA002JU24f"
/tissue_type="Larva"
/lab_host="E. coli"
/clone_lib="Apis mellifera"
/note="Vector: pCUTBAC-1; Site_1: HindIII; Site_2: NotI;
For more details on library preparation and sequence
analysis see
http://www.genome.clemson.edu/projects/stc/bee/AM_Ba/ To
order clones from this library see
http://www.genome.clemson.edu/orders "

BASE COUNT 227 a 134 c 156 g 207 t 4 others

Query Match 71.4%; Score 15; DB 28; Length 728;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACCTTGAAGTGA 20
|||||
Db 118 GAACCTTGAAGTGA 132

RESULT 7
BZ391656/c 842 bp DNA linear GSS 30-APR-2003
LOCUS
DEFINITION EINC064TR EI 10 12 KB Entamoeba invadens genomic clone EINC064,
genomic survey sequence.

ACCESSION BZ391656
VERSION BZ391656.1 GI:30238193
KEYWORDS GSS.

SOURCE Entamoeba invadens
ORGANISM Entamoeba invadens
Eukaryota; Entamoebidae; Entamoeba.

REFERENCE 1 (bases 1 to 842)
Loftus,B., Wang,Z., Roncaglia,P., Van Aken,S. and Fraser,C.
AUTHORS Gene discovery in the Entamoeba invadens genome
TITLE
JOURNAL Unpublished

```
COMMENT
Other GSSs: EINC064TF
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seq primer: TR
Clas: sheared ends.

FEATURES
source
1..842
/organism="Entamoeba invadens"
/mol_type="genomic DNA"
/strain="IP-1"
/db_xref="taxon:33085"
/clone="EINC064"
/clone_1fb="EI 10 12 KB"
/note="Vector: pHO2. Site 1: BstXI; Total genomic DNA was
isolated from early log phase trophozoites of E. invadens
IP-1 using a Qiagen plant DNA extraction kit. A shotgun
medium-size plasmid library (average insert size of 10 -
12 kb) was generated by random mechanical shearing of E.
invadens genomic DNA, repairing the ends of DNA fragments
with T4 polymerase, adding BstXI adaptors and ligating
into the BstXI site of a pUC-derived vector pHO2."

BASE COUNT
281 a 152 c 140 g 269 t

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTGAGATGAT 21
|||||
796 AACGTTGAGATGAT 782

Db

RESULT 8
CD375545 889 bp mRNA linear EST 31-MAY-2003
LOCUS CD375545
DEFINITION PTM00709 Phaeodactylum tricornutum Uni-Zap XR Phaeodactylum
tricornutum cDNA 5', mRNA sequence.
ACCESSION CD375545
VERSION CD375545.1 GI:31251159
KEYWORDS EST.
SOURCE Phaeodactylum tricornutum
ORGANISM Phaeodactylum tricornutum
Eukaryota; stramenopiles; Bacillariophyta; Bacillariophyceae;
Bacillariophycidae; Naviculales; Phaeodactylaceae; Phaeodactylum.
1 (bases 1 to 889)
Scala,S., Carels,N., Falciatore,A., Chiusano,M.L. and Bowler,C.
Genome properties of the diatom Phaeodactylum tricornutum
Plant Physiol. 129 (3), 993-1002 (2002)
2211123
1211455
12114555
Contact: Bowler C
Laboratory of Molecular Plant Biology
Stazione Zoologica 'Anton Dohrn'
Villa Comunale, I-80121, Napoli, Italy
Tel: 39 081 583 3268/3211
Fax: 39 081 764 1355
Email: christel@na.szn.it
Diatom EST Database(http://aves.thagen.sznbowlr.com)
Seq primer: T3 backward
POLYA=yes.

FEATURES
source
1..889
/organism="Phaeodactylum tricornutum"
/mol_type="mRNA"
/db_xref="taxon:2850"
/cell_line="CIMP632"

COMMENT
Other GSSs: EINC064TF
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seq primer: TR
Clas: sheared ends.

FEATURES
source
1..842
/organism="Entamoeba invadens"
/mol_type="genomic DNA"
/strain="IP-1"
/db_xref="taxon:33085"
/clone="EINC064"
/clone_1fb="EI 10 12 KB"
/note="Vector: pHO2. Site 1: BstXI; Total genomic DNA was
isolated from early log phase trophozoites of E. invadens
IP-1 using a Qiagen plant DNA extraction kit. A shotgun
medium-size plasmid library (average insert size of 10 -
12 kb) was generated by random mechanical shearing of E.
invadens genomic DNA, repairing the ends of DNA fragments
with T4 polymerase, adding BstXI adaptors and ligating
into the BstXI site of a pUC-derived vector pHO2."

BASE COUNT
281 a 152 c 140 g 269 t

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 87;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTGAGATGAT 21
|||||
796 AACGTTGAGATGAT 782

Db

RESULT 9
BX455352 913 bp mRNA linear EST 22-MAY-2003
LOCUS BX455352
DEFINITION BX455352 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CSDDP022YA13 3-PRIME, mRNA sequence.
ACCESSION BX455352
VERSION BX455352.1 GI:31019187
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 913)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10667.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDBAK038CA04NM2&cluster=10667.f. Contact :
Feng liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSDBAK038CA04NM2.

FEATURES
source
1..913
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDP022YA13"
/tissue_type="FETAL BRAIN"
/dev_stage="fetal"
/clone_1fb="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dt) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoR sites of the pCMVSPORT 6
vector. Library was not normalized."

BASE COUNT
304 a 199 c 163 g 246 t

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 88;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTGAGATGA 20
|||||
900 GAACGTTGAGATGA 886

Db

RESULT 10
CC235774 1220 bp DNA linear GSS 12-MAY-2003
LOCUS CC235774
DEFINITION CH261-139L19_RM1.2 CH261 Gallus gallus genomic clone CH261-139L19,
```

genomic survey sequence.
ACCESSION CC235774
VERSION CC235774.1 GI:30562437
KEYWORDS GSS.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1220)
Krentzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J.,
Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus gallus BAC End Reads
TITLE Unpublished
JOURNAL
COMMENT Contact: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 18200 Std Error: 0.00
Seq primer: RML TACGACTCAGCTATGAGGAGA
Class: BAC ends
High quality sequence start: 473
High quality sequence stop: 541.
Location/Qualifiers
1..1220
/organism="Gallus gallus"
/mol_type="genomic DNA"
/strain="Red Jungle Fowl"
/db_xref="taxon:9031"
/clone="CH261-139A19"
/sex="female"
/cell_line="VCD001, inbred 256"
/clone_1ib="CH261"
/note="Vector: PTARBAC2.1; Site 1: EcorI; Site 2: EcorI;
CH261 Female Chicken library - for library and clone
ordering information: <http://www.chori.org/bacpac>"

BASE COUNT 320 a 330 c 171 g 399 t
ORIGIN

Query Match 71.4%; Score 15; DB 29; Length 1220;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTCCGAGATGAT 21
|||||
461 AACGTTCCGAGATGAT 447

Db

RESULT 11 108 bp mRNA linear HTC 08-JAN-2003
CNS09N54
LOCUS CNS09N54/c
DEFINITION Single read from an extremity of a full-length cDNA clone made from
Anopheles gambiae total adult females. 5-PRIME end of clone
FK0A05AH09 of strain 6-9 of Anopheles gambiae (African malaria
mosquito).
ACCESSION BX066068
VERSION BX066068.1 GI:27639349
KEYWORDS HTC.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 108)
Genoscope.
Direct Submission
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
Location/Qualifiers
1..108
/organism="Anopheles gambiae"
/mol_type="mRNA"

FEATURES
source

/strain="6-9"
/db_xref="taxon:7165"
/clone="FK0A05AH09"
/plasmid="pME18-FL"
/note="end : 5-PRIME"

BASE COUNT 21 a 31 c 34 g 22 t
ORIGIN

Query Match 66.7%; Score 14; DB 11; Length 108;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAACGTTCCGAGAT 18
|||||
Db 61 CGAACGTTCCGAGAT 48

RESULT 12 168 bp mRNA linear EST 31-MAR-1995
R04873
LOCUS pk33h10.r1 Kuwabara Mixed stage C. briggsae Caenorhabditis briggsae
DEFINITION cDNA, mRNA sequence.
ACCESSION R04873
VERSION R04873.1 GI:754609
KEYWORDS EST.
SOURCE Caenorhabditis briggsae
ORGANISM Caenorhabditis briggsae
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 168)
Hillier, L., Chippelli, B., Chisase, S., Clark, N., Couch, J., Dubuque
T., Hawkins, M., Holtman, M., Holtman, M., Kucaba, T., Kuwabara, P., Le
M., Mardis, E., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Tan
F., Treviski, E., Waterston, R., Wohlmann, P. and Wilson, R.
Washington University Caenorhabditis briggsae EST project
TITLE Unpublished
JOURNAL
COMMENT Contact: Marra MA
Washington University Genome Sequencing Center
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1455
Fax: 314 286 1810
Email: mmarra@watson.wustl.edu
PCR F: TGTAACAGCAGCGCAGTAGCAGTTCAGCTCG
PCR B: CAGGAACAGCTATGACCTTATGACTATTTCTTCAGGATA
Source: Washington University Genome Sequencing Center
PCR amplified DNA is available from Washington University Genome
Sequencing Center. Aliquots of the library may be requested from P.
Kuwabara (pek@wrc-lmb.cam.ac.uk).
Seq primer: Commercially available M13 reverse dye primer.
Location/Qualifiers
1..168
/organism="Caenorhabditis briggsae"
/mol_type="mRNA"
/strain="G16 Gujarat"
/db_xref="taxon:6238"
/clone_1ib="Kuwabara Mixed stage C. briggsae"
/note="Vector: Lambda gT10; Site 1: EcorI; Site 2: EcorI;
Stage:mixed. Sex:hermaphrodite. Library construction:
First strand oligo(dT) primed. Second strand was as per
Gubler/Hofman. Ligated to EcorI adaptors. Library is
non-directional. Library is non-normalized. Library
constructed by P.E. Kuwabara. Additional details on
construction of the library are described in P.E.
Kuwabara and S. Shah, NAR 22: 4414 - 4418 (1994). Adaptor
sequence: GAATTC CGTTGCTGTCG"

BASE COUNT 46 a 42 c 42 g 38 t
ORIGIN

Query Match 66.7%; Score 14; DB 14; Length 168;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGACGCTCG 14
 |||||
 Db 148 TCGTCGACGCTCG 161

RESULT 13
 AA186214/c 298 bp mRNA linear EST 10-JAN-1997
 LOCUS T3860 MWAT4 bloodstream form of serodeme WRATat1.1 Trypanosoma
 DEFINITION brucei rhodesiense cDNA 5', mRNA sequence.
 ACCESSION AA186214
 VERSION AA186214.1 GI:1772670
 KEYWORDS EST.
 SOURCE Trypanosoma brucei rhodesiense
 ORGANISM Trypanosoma brucei rhodesiense
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE
 AUTHORS Djikeng, A., Donelson, J.E. and Majiwa, P.A.O.
 TITLE Generation of expressed sequence tags as physical landmarks in the
 genome of Trypanosoma brucei
 JOURNAL Unpublished
 COMMENT Contact: Majiwa PAO
 Molecular Biology Unit
 International Livestock Research Institute
 P.O. Box 30709, Nairobi, Kenya
 Tel: 254-2 630743
 Fax: 254-2 631499
 Email: p.majiwa@cnet.com
 Seq primer: T3 primer.
 Location/Qualifiers

FEATURES
 source
 1..298
 /organism="Trypanosoma brucei rhodesiense"
 /mol_type="mRNA"
 /sub_species="rhodesiense"
 /db_xref="taxon:31286"
 /clone_lib="MWAT4 bloodstream form of serodeme WRATat1.1"
 /note="Vector: lambda ZAP II (Stratagene); Site 1: EcoRI;
 Site 2: XhoI; The mRNA was purified from a cloned
 population of bloodstream trypanosomes reexpressing the
 MWAT4 metacyclic variant surface glycoprotein (VSG). A
 unidirectional oligo dT-primed EcoRI/XhoI cDNA library was
 constructed in lambda ZAP II (Stratagene)."

BASE COUNT 93 a 63 c 86 g 56 t
 ORIGIN

Query Match 66.7%; Score 14; DB 9; Length 298;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACGTTCGAGATGAT 21
 |||||
 Db 263 ACGTTCGAGATGAT 250

RESULT 14
 CNS09090/c 348 bp mRNA linear HTC 08-JAN-2003
 LOCUS Single read from an extremity of a full-length cDNA clone made from
 DEFINITION Anopheles gambiae total adult females. 5-PRIME end of clone
 FK0AAGTAB01 of strain 6-9 of Anopheles gambiae (African malaria
 mosquito).
 ACCESSION BX070056
 VERSION BX070056.1 GI:27643377
 KEYWORDS HTC.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.
 REFERENCE 1 (bases 1 to 348)
 AUTHORS Genoscope.
 TITLE Direct Submission

JOURNAL
 Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 Evry cedex - FRANCE (E-mail : sequef@genoscope.cns.fr)
 - Web : www.genoscope.cns.fr

FEATURES
 source
 1..348
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="6-9"
 /db_xref="taxon:7165"
 /clone="FK0AAGTAB01"
 /plasmid="pME185-PL"
 /note="end : 5-PRIME"

BASE COUNT 81 a 101 c 114 g 52 t
 ORIGIN

Query Match 66.7%; Score 14; DB 11; Length 348;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGACGTCGAGAT 18
 |||||
 Db 263 CGACGTCGAGAT 250

RESULT 15
 B1507844 387 bp mRNA linear EST 08-APR-2002
 LOCUS BBI70008B10E04.5 Bee Brain Normalized/Subtracted Library, BBI7 Apis
 DEFINITION mellifera cDNA clone BBI70008B10E04 5', mRNA sequence.
 ACCESSION B1507844
 VERSION B1507844.1 GI:15358218
 KEYWORDS EST.
 SOURCE Apis mellifera (honeybee)
 ORGANISM Apis mellifera
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Hymenoptera; Apoidea; Aculeata; Apoidea;
 Apidae; Apis.

REFERENCE
 AUTHORS Whitfield, C.W., Band, M.R., Bonaldo, M.F., Kumar, C.G., Liu, L.,
 Partins, J., Robertson, H.M., Soares, B. and Robinson, G.E.
 TITLE Annotated expressed sequence tags and cDNA microarrays for studies
 of brain and behavior in the honey bee
 JOURNAL Genome Res. 12 (4), 555-566 (2002)
 MEDLINE 21929762
 PUBMED 11932240

COMMENT
 Contact: Gene E. Robinson
 Department of Entomology
 University of Illinois
 505 S. Goodwin Ave., Urbana, IL 61801, USA
 Tel: 217 265 0309
 Fax: 217 244 3493
 Email: gene@life.uiuc.edu
 This research was funded by the University of Illinois Critical
 Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
 Award in Functional Genomics to G.E. Robinson and an NSF
 postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
 PCR PRIMERS
 FORWARD: TAAATACACTGACTATAGCG
 BACKWARD: ATTATCCCTCACTAAG
 Plate: BBI70008B10 row: 5 column: 04
 Seq primer: AGCGATACCAATTTCACACAGA
 High quality sequence stop: 387.
 Location/Qualifiers

FEATURES
 source
 1..387
 /organism="Apis mellifera"
 /mol_type="mRNA"
 /strains="mixed strains of European bees, predominantly
 A.m. ligustica"
 /db_xref="taxon:7460"
 /clone="BBI70008B10E04"
 /sex="female"
 /tissue_type="brain"
 /dev_stage="adult worker honey bee"

clone.lib="bee Brain Normalized/Subtracted Library, BBL7
/note=Organ: brain; Vector: pT7T3-Pac; Site 1: EcoRI;
Site 2: NotI; This BBL7 cDNA library was generated by
subtraction of the BBL6 library with 4000 previously
sequenced clones. The BBL6 library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lemon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806. RNA was
prepared from dissected brains of adult worker bees of
various ages and various behavioral groups. "

BASE COUNT ORIGIN	99 a	100 c	104 g	110 t	1 others
----------------------	------	-------	-------	-------	----------

Query Match	66.7%	Score 14	DB 12	Length 414
Best Local Similarity	100.0%	Pred. No. 3.1e+02		
Matches 14	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```

QY      5 CGAACGTCGAGAT 18
          |||||
Db      164 CGAACGTCGAGAT 177

```

RESULT 17				
CB333691	CB333691	424 bp	mRNA	linear
LOCUS				
DEFINITION	TgESTzyl67b10.y1 TgME49 B7 Tachyzoite CDNA Library 2 Toxoplasma			
ACCESSION	gondii cDNA clone TgESTzyl67b10.y1 5', mRNA sequence.			
	CB333691			

ACCESSION CB333691
VERSION CB333691.1 GI:28915374
KEYWORDS EST.
SOURCE Toxoplasma gondii
ORGANISM Toxoplasma gondii
Bukaryota; Alveolate; Apicomplexa; Coccidia; Eimeriida

REFERENCE
AUTHORS
1 (bases 1 to 424)
Sarcocystidae; Toxoplasma.
Tang,K., Cole,R., Fogarty,S., Sibley,L.D., Ajikwa,J.A., White,M.,
Clifton,S., Pape,D., Martin,J., Wylie,T., Dante,M., Marra,M.,
Hillier,L., Kucaba,T., Theising,B., Bowers,Y., Gibbons,M., Ritzer
,S., Bennett,J., Franklin,C., Tsagarisavlili,R., Ronko,I., Kennedy
,S., Maguire,L., Waterson,K. and Wilson,R.
Toxoplasma EST Project
TITLE
JOURNAL
Unpublished

TITLE
Toxoplasma EST Project
JOURNAL
Unpublished
COMMENT
Contact: Clifton, S.
Toxoplasma EST Project
Washington University School of Medicine

Email: toxco@watson.wustl.edu for further
Contact David Sibley (toxcoes@borcim.wustl.edu)
information relating to organism, libraries, or clone availability
Seq primer: -40RP from Glbco.
Location/Qualifiers
1. .424
/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
/clone="IGBSTzyf67b10.y1"
/dev_stage="tachyzoite"
/lab_host="E. coli XL10"
/clone_lib="TGM89 B7 Tachyzoite cDNA library 2"

```

/organism="Toxoplasma gondii"
/mol_type="mRNA"
/db_xref="taxon:5811"
/clone="TGSTzyf67b10.y1"
/dev_stage="tachyzoitea"
/lab_host="E.coli XL10"
/clone_lib="TgM49 B7 Tachyzo"
/note="Vector: pBluescript II
ECor1. The cDNA library was c

```

synthesized from poly mRNA using an oligo-dT primer containing a XhoI site. Following second strand synthesis EcoRI adapters were ligated to the cDNA, and products were size-selected on sephacryl S500. The cDNA were directionally cloned into the EcoRI/XhoI prepared pBluescript II SK+ vector, and transformed into XL10 cells (Stratagene). The library may contain a small percentage of host or bacterial contaminants."

ORIGIN

Query Match 66.7%; Score 14; DB 14; Length 424;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGAACGTTTCG 14
 |||||
 Db 123 TCGTCGAACGTTTCG 136

RESULT 18
 BM629296 433 bp mRNA linear EST 26-FEB-2002
 LOCUS BM629296/c
 DEFINITION 17000687499932 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 19600449650107 5', mRNA sequence.
 ACCESSION BM629296
 VERSION BM629296.1 GI:18928807
 SOURCE EST.
 ORGANISM Anopheles gambiae (African malaria mosquito)
 Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.
 1 (bases 1 to 433)
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
 R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 Celerera Anopheles gambiae EST project
 TITLE Celerera Anopheles gambiae EST project
 JOURNAL Unpublished
 COMMENT Contact: Holt R.A.
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltR@cclera.com
 Plate: NU01004AZR row: K column: 01
 Seq primer: M13 Reverse.
 Location/Qualifiers

FEATURES
 source 1..433
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced suscep. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449650107"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /clone_1lb="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.
 cDNA inserts >500 bp cloned directionally into pSport 1.
 Not 1 site is 3'. Clones available through the Malaria
 Research and Reference Reagent Resource Center
 (www.malaria.mr4.org)."

BASE COUNT 111 a 109 c 137 g 76 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 433;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAAGCTCGAGAT 18
 |||||
 Db 426 CGAAGCTCGAGAT 413

RESULT 19
 AQ252378 439 bp DNA linear GSS 10-OCT-1998
 LOCUS AQ252378
 DEFINITION HS_2262_A2_H06_MR_CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=2262 Col=12 Row=O, genomic survey
 sequence.
 ACCESSION AQ252378

VERSION AQ252378.1 GI:3722551
 GSS.
 KEYWORDS Homo sapiens (human)
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 439)
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., and
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 JOURNAL MEDLINE 99380589
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Sequence Tagged Connector
 Plate: 2262 row: O column: 12
 Class: BAC ends
 High quality sequence stop: 439.
 Location/Qualifiers

FEATURES
 source 1..439
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=2262 Col=12 Row=O"
 /sex="male"
 /clone_1lb="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelBAC11; BAC Clones in
 E-Coli DH10B"

BASE COUNT 140 a 80 c 95 g 121 t 3 others

ORIGIN

Query Match 66.7%; Score 14; DB 28; Length 439;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAAGCTCGAGATG 19
 |||||
 Db 113 GAAGCTCGAGATG 126

RESULT 20
 CA302582 466 bp mRNA linear EST 01-NOV-2002
 LOCUS CA302582
 DEFINITION taal3b12.x1 Hydra cDNA library Hydra magnipapillata cDNA 3', mRNA
 sequence.
 ACCESSION CA302582
 VERSION CA302582.1 GI:24465641
 EST.
 SOURCE Hydra magnipapillata
 Hydra magnipapillata
 Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydrozoa; Anthomedusae;
 Hydridae; Hydra.
 1 (bases 1 to 466)
 Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,
 Martinez, D., Kibler, D., Hampson, S., Clifton, S., Page, D., Marra, M.,
 Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y.,
 Gibbons, M., Ritzer, E., Bennett, J., Ronko, I., Tsagaris, V., R.,
 Maguire, L., Kennedy, S., Waterston, R. and Wilson, R.
 Washu Hydra EST Project
 TITLE Washu Hydra EST Project
 JOURNAL Unpublished
 COMMENT Other ESTs: taal3b12.y1
 Contact: Hans Bode
 Washu Hydra EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 Library was constructed by H. Bode and B. Blumberg DNA sequencing
 by: Washington University Genome Sequencing Center For information
 on obtaining a clone please contact: Hans Bode (hbode@wustl.edu)
 Seq primer: Primer name ambiguous
 High quality sequence stop: 426.
 Location/Qualifiers

FEATURES

source

1..466

/organism="Hydra magnipapillata"

/mol_type="mRNA"

/db_xref="taxon:6085"

/lab_host="Hydra CDNA library"

/clone_lib="PSORT6; Site 1: NotI; Site 2: SalI;

libraries prepared by Phil Wigge, Plant Molecular and

Cellular Biology, Lab (Detlev Weigel), The Salk Institute

for Biological Science, 10010 North Torrey Pines Road, La

Jolla, CA 92037."

BASE COUNT

144 a 82 c 73 g 167 t

ORIGIN

Query Match 66.7%; Score 14; DB 14; Length 466;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTTCCGAGATGA 20

Db 106 AACGTTCCGAGATGA 93

RESULT 21

LOCUS

CNS09GNZ/C

DEFINITION 469 bp mRNA linear HTC 08-JAN-2003

Single read from an extremity of a full-length cDNA clone made from

Anopheles gambiae total adult females. 5-PRIME end of clone

FK0AC37DA02 of strain 6-9 of Anopheles gambiae (African malaria

mosquito).

VERSION BX057675.1 GI:27630956

KEYWORDS HTC.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;

Anopheles.

REFERENCE 1 (bases 1 to 469)

AUTHORS Genoscope.

TITLE Direct Submission

JOURNAL Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

FEATURES Location/Qualifiers

source 1..469

/organism="Anopheles gambiae"

/mol_type="mRNA"

/strain="6-9"

/db_xref="taxon:7165"

/clone="FK0AC37DA02"

/plasmid="pME18S-FL"

/note="end : 5-PRIME"

BASE COUNT 115 a 126 c 157 g 71 t

ORIGIN

Query Match 66.7%; Score 14; DB 11; Length 469;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTG 14

Db 214 TCGTGAACGTTG 201

RESULT 22

LOCUS

AA097939

DEFINITION

484 bp mRNA linear EST 15-FEB-1997

ma2901.r1 Stratiene mouse Tcell 937311 Mus musculus cDNA clone

IMAGE:550608 5' similar to gb:X69392.608 RIBOSOMAL PROTEIN L26

(HUMAN); gb:X80699 M.musculus L26 mRNA (MOUSE);, mRNA sequence.

AA097939

VERSION

AA097939.1 GI:1643492

KEYWORDS

EST.

SOURCE

Mus musculus

ORGANISM

Mus musculus (house mouse)

REFERENCE

1 (bases 1 to 484)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisler,S., Kucaba,T., Lacy,M., Le,M., Martin,D., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.

THE WASHU-HHMI MOUSE EST PROJECT

Unpublished

CONTACT: Marra M/Mouse EST Project

Washington University School of Medicine

444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MG1:331400

Seq primer: -28m13 rev1 ET from Amerham

High quality sequence stop: 7.

LOCATION/Qualifiers

1..484

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:550608"

/tissue_type="Tcell"

/dev_stage="M30 CD4+ cells"

/lab_host="SOAR (kanamycin resistant)"

/clone_lib="Stratiene mouse Tcell 937311"

/note="Organ: blood; Vector: plasmid SK-; Site 1:

ECORI; Site 2: XhoI; Cloned unidirectionally. Primer:

Oligo dr. M30 CD4+ cells. Average insert size: 1.0 kb;

Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTGGCGACGAG

3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTT 3'."

BASE COUNT 142 a 128 c 115 g 99 t

ORIGIN

Query Match 66.7%; Score 14; DB 9; Length 484;

Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACGTTCGAGATGAT 21

Db 424 ACGTTCGAGATGAT 437

RESULT 23

LOCUS

BM636144

DEFINITION

486 bp mRNA linear EST 26-FEB-2002

17000687561542 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone

IMAGE:550608 5' mRNA sequence.

BM636144

VERSION

BM636144.1 GI:18935655

KEYWORDS

EST.

SOURCE

Anopheles gambiae (African malaria mosquito)

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;

REFERENCE 1 (bases 1 to 486)
 AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
 TITLE R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 JOURNAL Celera Anopheles gambiae EST project
 COMMENT Unpublished
 Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltR@celera.com
 Plate: NU01004922 row: N column: 16
 Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1..486
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449644818"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_1ib="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.
 cDNA inserts >500 bp cloned directionally into pSport 1.
 Not 1 site is 3'. Clones available through the Malaria
 Research and Reference Reagent Resource Center
 (www.malaria.mr4.org)."
 BASE COUNT 119 a 129 c 156 g 82 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 486;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18
 |||||
 Db 387 CGAAGCTTCGAGAT 374

RESULT 24
 LOCUS BM652631 492 bp mRNA linear EST 26-FEB-2002
 DEFINITION 17000687313490 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 19600449634767 5', mRNA sequence.
 ACCESSION BM652631
 VERSION BM652631.1 GI:18952142
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles
 1 (bases 1 to 492)
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
 R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 Celera Anopheles gambiae EST project
 Unpublished
 Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltR@celera.com
 Plate: NU01004922 row: K column: 21
 Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1..492
 /organism="Anopheles gambiae"
 /mol_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449634767"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_1ib="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.
 cDNA inserts >500 bp cloned directionally into pSport 1.
 Not 1 site is 3'. Clones available through the Malaria
 Research and Reference Reagent Resource Center
 (www.malaria.mr4.org)."
 BASE COUNT 117 a 134 c 157 g 84 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 492;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18
 |||||
 Db 440 CGAAGCTTCGAGAT 427

RESULT 25
 LOCUS BM644091 493 bp mRNA linear EST 26-FEB-2002
 DEFINITION 17000687313490 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 19600449671469 5', mRNA sequence.
 ACCESSION BM644091
 VERSION BM644091.1 GI:18943602
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles
 1 (bases 1 to 493)
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
 R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 Celera Anopheles gambiae EST project
 Unpublished
 Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltR@celera.com
 Plate: NU01004922 row: E column: 03
 Seq primer: M13 Reverse.

FEATURES

source

Location/Qualifiers

1..493
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449671469"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_1ib="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.
 cDNA inserts >500 bp cloned directionally into pSport 1.
 Not 1 site is 3'. Clones available through the Malaria
 Research and Reference Reagent Resource Center
 (www.malaria.mr4.org)."

BASE COUNT

120 a 129 c 159 g 85 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 493;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CGAAGCTTCGAGAT 18
 |||||
 Db 398 CGAAGCTTCGAGAT 385

RESULT 26
 BM597612/c 499 bp mRNA linear EST 25-FEB-2002
 LOCUS 17000687499086 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
 DEFINITION 19600449683979 5', mRNA sequence.

ACCESSION BM597612
 VERSION BM597612.1 GI:18895703
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.

REFERENCE 1 (bases 1 to 499)
 AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
 TITLE R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 JOURNAL Celerera Anopheles gambiae EST project
 COMMENT Unpublished
 Contact: Holt R.A.
 Celerera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRa@celerera.com
 Plate: NU01004B2S row: M column: 21
 Seq primer: M13 Reverse.

FEATURES
 source location/Qualifiers

1..499
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449683979"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_1ib="A.Gam.ad.cDNA.blood1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
 hours after human blood feeding. cDNA inserts >500 bp
 cloned directionally into pSport 1. Not 1 site is 3'.
 Clones available through the Malaria Research and
 Reference Reagent Resource Center (www.malaria.mr4.org)"
 BASE COUNT 121 a 131 c 159 g 88 t

Query Match 66.7%; Score 14; DB 12; Length 499;
 Best Local Similarity 100.0%; Pred. No. 3.1e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CGAAGCTTCGAGAT 18
 |||||
 Db 428 CGAAGCTTCGAGAT 415

RESULT 27
 BM611518/c 504 bp mRNA linear EST 25-FEB-2002
 LOCUS 17000687115945 A.Gam.ad.cDNA.blood1 Anopheles gambiae cDNA clone
 DEFINITION 19600449722493 5', mRNA sequence.

ACCESSION BM611518
 VERSION BM611518.1 GI:18909622
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.
 REFERENCE 1 (bases 1 to 504)
 AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
 TITLE R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 JOURNAL Celerera Anopheles gambiae EST project
 COMMENT Unpublished
 Contact: Holt R.A.
 Celerera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRa@celerera.com
 Plate: NU01004A9Y row: B column: 15
 Seq primer: M13 Reverse.

FEATURES
 source location/Qualifiers

1..504
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449722493"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_1ib="A.Gam.ad.cDNA.blood1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
 hours after human blood feeding. cDNA inserts >500 bp
 cloned directionally into pSport 1. Not 1 site is 3'.
 Clones available through the Malaria Research and
 Reference Reagent Resource Center (www.malaria.mr4.org)"
 BASE COUNT 123 a 132 c 161 g 88 t

Query Match 66.7%; Score 14; DB 12; Length 504;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 5 CGAAGCTTCGAGAT 18
 |||||
 Db 426 CGAAGCTTCGAGAT 413

RESULT 28
 BM866297 512 bp mRNA linear EST 06-MAY-2003
 LOCUS mgc8005xk24f.b Magnaporthe grisea CS Uni-Zap XR library Magnaporthe
 DEFINITION grisea cDNA clone mgc8005xk24 5', mRNA sequence.

ACCESSION BM866297
 VERSION BM866297.2 GI:30394811
 KEYWORDS EST.
 SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
 ORGANISM Magnaporthe grisea
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.

REFERENCE 1 (bases 1 to 512)
 AUTHORS Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G., Bhatterai
 TITLE K. and Dean,R.A.
 JOURNAL Expressed sequence tags from the rice blast fungus, Magnaporthe
 grisea
 COMMENT Unpublished
 On Mar 7, 2002 this sequence version replaced gi:19233979.
 Contact: Ebbole DJ
 Department of Plant Pathology & Microbiology
 Texas A&M University
 Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
 Tel: 979 845 4831
 Fax: 979 845 6483
 Email: d-ebbole@tamu.edu

Chromatogram file of this sequence is available, see contact person
 'Best nr hit (April. 22, 2003) gb|EAA28529.1| hypothetical protein
 [Neurospora crassa] 107 9e-49

PCR Primers
 FORWARD: T3 primer
 BACKWARD: T7 primer
 Plate: mgc805 row: E column: 24
 Seq primer: T3.
 Location/Qualifiers
 1. 512

FEATURES
 source
 /organism="Magnaporthe grisea"
 /mol_type="rRNA"
 /strain="Guy11"
 /db_xref="taxon:148305"
 /clone="mgc805x24"
 /sex="Mat1-2 hermaphrodite"
 /cell_type="conidia"
 /clone_lib="Magnaporthe grisea CS Uni-Zap XR Library"
 /note="Vector: pBluescriptSK-, Site_1: EcoRI, Site_2: XhoI
 ; Unidirectional cloning. EcoRI site has T3 primer and
 predominantly 5' reads. T7 primer on XhoI side of insert.
 Conidia library. Point inoculation of Guy11 at center of
 oatmeal agar plate. Conidia were harvested after two weeks
 of growth. Sequences were processed by one of two methods.
 Where a full-length alignment to the M. grisea genome
 sequence was available, the EST sequence was trimmed
 according to the alignment, otherwise sequence quality was
 assessed using phredphrap version 991019 and trimmed
 according to phd files (0.05) and for vector seqs."
 BASE COUNT 118 a 161 c 119 g 114 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 512;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACGTTCCAGATGA 20
 |||||
 356 AACGTTCCAGATGA 369

RESULT 29
 LOCUS CB358730 513 bp mRNA linear EST 17-MAR-2003
 DEFINITION ZF001-P00024-DPE-F-A G12 GISZF001 Dario xerio cDNA clone
 IMAGE:5900672 5' similar to fc24g12.y1 Zebrafish Washu M71MG EST
 Dario xerio cDNA clone IMAGE:3722374 5' mRNA sequence.
 ACCESSION CB358730.1 GI:29001661
 VERSION CB358730.1
 KEYWORDS EST.
 SOURCE Dario xerio (zebrafish)
 ORGANISM Dario xerio

REFERENCE
 AUTHORS Mathavan,S., Wei,C., Thoreau,H., Chia,J.M. and Ruan,Y.
 TITLE 1 (bases 1 to 513)
 JOURNAL Cyprinidae; Dario.
 COMMENT Unpublished
 Contact: Ruan Y
 Laboratory of Molecular Biotechnology
 Genome Institute of Singapore
 1 Science Park Road, The Capricorn #05-01, Singapore 117528
 Tel: +65 6827 5200
 Fax: +65 6827 5201
 Email: gisry@nus.edu.sg
 GIS Clone ID: ZF001-P00024-PP_M23
 PCR Primers
 FORWARD: M13
 BACKWARD: M13
 Plate: ZF001-P00024-DPE-F-A
 Seq primer: CCGCACTTACTTATAGCA
 High quality sequence scop: 513.
 Location/Qualifiers
 1. 513
 /organism="Dario xerio"

FEATURES
 source
 /mol_type="rRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:6900672"
 /tissue_type="embryo"
 /dev_stage="7 Different embryonic Stages (From just
 fertilized Embryos to 72 hours just hatched baby fish)"
 /lab_host="DH10B"
 /clone_lib="GISZF001"
 /note="Vector: pDMR-LIB; Site_1: Sfi A (GGCATTACGGCC);
 Site_2: Sfi B (GGCCGCTCGGCC); Priming method: Sfi (dT)30
 primed; Priming sequence: 5'ATTCTAGA GGCCGAGCGGCC
 GACATG(7)30VN; Directionally cloned, 5' cloning site:
 Sfi A site GGCCATTACGGCC; 5' linker/adaptor sequence:
 5.AAGCATGGATCAACGACGAGTGGCC; 3' cloning site: Sfi B
 site GGCCGCTCGGCC; 3' linker/adaptor sequence: same
 as the priming sequence; Average insert size: 2kb; For
 PCR insert analysis: Use M13 forward and reverse primers;
 Library Amplified Recombinants (inserts): 984; Library
 complexity: 5x10⁶; Full-length construction (method):
 SMART, a Clontech method; Library constructed by: S.
 Mathavan, Chia-Lin Wei, and Yijun Ruan Genome Institute of
 Singapore"
 BASE COUNT 131 a 108 c 112 g 162 t
 ORIGIN

Query Match 66.7%; Score 14; DB 14; Length 513;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACGTTCCAGATGA 20
 |||||
 422 AACGTTCCAGATGA 435

RESULT 30
 LOCUS BH899325 521 bp DNA linear GSS 30-AUG-2002
 DEFINITION Ot060392 Ostreococcus tauri genomic shotgun library Ostreococcus
 tauri genomic clone otaz23a09.D 5', genomic survey sequence.
 ACCESSION BH899325.1 GI:22550820
 VERSION BH899325.1
 KEYWORDS GSS.
 SOURCE Ostreococcus tauri
 ORGANISM Ostreococcus tauri

REFERENCE
 AUTHORS Derelle,E., Ferraz,C., Lagoda,P., Eychenne,S., Cooke,R., Regad,F.,
 1 (bases 1 to 521)
 JOURNAL Mammaliaceae; Ostreococcus.
 COMMENT Unpublished
 Contact: Moreau H
 Laboratoire Arago
 CNRS UMR 7628
 BP 44, Avenue Fontaule, 66651 Banyuls sur mer, France
 Tel: (33)468887309
 Fax: (33)468887398
 Email: h.moreau@obs-banyuls.fr
 Seq primer: forward
 Class: Shotgun.
 Location/Qualifiers
 1. 521
 /organism="Ostreococcus tauri"
 /mol_type="genomic DNA"
 /strain="OTTH0595"
 /db_xref="taxon:70448"
 /clone="ota23a09.D"
 /clone_lib="Ostreococcus tauri genomic shotgun library"
 /note="Vector: Bluescript; Site_1: EcoRV; Site_2: EcoRV;
 Shotgun library prepared after ionization of the genomic

FEATURES
 source

DNA. Blunt ligation in EcoRV site of Bluescript. Size selection of the inserts after agarose electrophoresis between 1 and 3 kb."

BASE COUNT 84 a 146 c 214 g 77 t

ORIGIN

Query Match 66.7%; Score 14; DB 28; Length 521;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGTCGACGTCGAT 15

|||||

Db 77 CGTCGACGTCGAT 90

RESULT 31

LOCUS BM618536 527 bp mRNA linear EST 25-FEB-2002

DEFINITION 17000687439164 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone

19600449662307 5', mRNA sequence.

ACCESSION BM618536

VERSION BM618536.1 GI:18916954

KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.

REFERENCE 1 (bases 1 to 527)

Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab R., Collins,F.H., Venter,J.C. and Hoffman,S.L.

Celera Anopheles gambiae EST project

Unpublished

Contact: Holt R.A.

Celera Genomics

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NU01004185 row: G column: 09

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..527

/organism="Anopheles gambiae"

/mol_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"

/db_xref="taxon:7165"

/clone="19600449662307"

/dev_stage="Adult"

/lab_host="DH10b"

/clone_1lb="A.Gam.ad.cDNA1"

/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

BASE COUNT 125 a 138 c 174 g 90 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 527;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTCGAGAT 18

|||||

Db 450 CGACGTCGAGAT 437

RESULT 32

LOCUS BM618261 528 bp mRNA linear EST 25-FEB-2002

DEFINITION 17000687437986 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone

19600449620529 5', mRNA sequence.

ACCESSION BM618261

VERSION BM618261.1 GI:18916553

KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.

REFERENCE 1 (bases 1 to 528)

Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab R., Collins,F.H., Venter,J.C. and Hoffman,S.L.

Celera Anopheles gambiae EST project

Unpublished

Contact: Holt R.A.

Celera Genomics

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NU01004NAK row: J column: 15

Seq primer: M13 Reverse.

FEATURES

Location/Qualifiers

1..528

/organism="Anopheles gambiae"

/mol_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"

/db_xref="taxon:7165"

/clone="19600449620529"

/dev_stage="Adult"

/lab_host="DH10b"

/clone_1lb="A.Gam.ad.cDNA1"

/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."

BASE COUNT 127 a 141 c 168 g 92 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 528;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTCGAGAT 18

|||||

Db 438 CGACGTCGAGAT 425

RESULT 33

LOCUS BM632494 528 bp mRNA linear EST 26-FEB-2002

DEFINITION 17000687504372 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone

19600449666961 5', mRNA sequence.

ACCESSION BM632494

VERSION BM632494.1 GI:18932005

KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.

REFERENCE 1 (bases 1 to 528)

Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab R., Collins,F.H., Venter,J.C. and Hoffman,S.L.

Celera Anopheles gambiae EST project

Unpublished

Contact: Holt R.A.

Celera Genomics

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004HMK row: I column: 07
 Seq primer: M13 Reverse.
 Location/Qualifiers

FEATURES

1..528

/organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
 /db_xref="taxon:7165"
 /clone="196004496179561"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.m4.org)."
 (www.malaria.m4.org).

BASE COUNT 123 a 136 c 168 g 101 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 528;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAAGCTTCGAGAT 18
 |||||
 Db 468 CGAAGCTTCGAGAT 455

RESULT 34 528 bp DNA linear GSS 13-DEC-2000
 TA99D10P
 LOCUS T. brucei sheared genomic DNA clone 99d10, forward sequence,
 DEFINITION genomic survey sequence.
 ACCESSION AL460276 GI:11862154
 VERSION AL460276
 KEYWORDS GSS.
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.

REFERENCE 1 (bases 1 to 528)
 AUTHORS Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
 Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
 Melville, S.E., Rajandream, M.A. and Barrett, B.G.
 TITLE Direct Submission

JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
 project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
 nh@sanger.ac.uk
 COMMENT Constructed at the Institute for Genomic Research (TIGR),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
 to give a tight size distribution (

4 kb). The v + i method used for the library construction is
 described in detail in Smith, H. and Venter, J.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds. M. Vaubin and B.
 Barrell, Oxford University Press, 1999).
 Email: nelsayed@tigr.org
 Details of T. brucei sequencing at the Sanger Centre are available
 at http://www.sanger.ac.uk/Projects/T_brucei/.

FEATURES

1..528 Location/Qualifiers

/organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927"
 /db_xref="taxon:5691"

BASE COUNT 116 a 177 c 118 g 117 t
 ORIGIN

Query Match 66.7%; Score 14; DB 29; Length 528;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGACGTTTCG 14
 |||||
 Db 29 TCGTCGACGTTTCG 42

RESULT 35 533 bp mRNA linear EST 26-FEB-2002
 BM641866/c
 LOCUS 17000687308831 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 DEFINITION 19600449617956 5', mRNA sequence.
 ACCESSION BM641866
 VERSION BM641866.1 GI:18941377
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.

REFERENCE 1 (bases 1 to 533)
 AUTHORS Holt, R.A., Lin, D.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
 , R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 TITLE Celera Anopheles gambiae EST project
 JOURNAL Unpublished
 COMMENT Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004HMK row: O column: 10
 Seq primer: M13 Reverse.
 Location/Qualifiers

FEATURES 1..533
 source /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449617956"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.m4.org)."
 (www.malaria.m4.org).

BASE COUNT 139 a 147 c 173 g 74 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 533;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAAGCTTCGAGAT 18
 |||||
 Db 336 CGAAGCTTCGAGAT 323

RESULT 36 534 bp DNA linear GSS 17-MAR-1999
 AQ407920
 LOCUS HS 5055_B2 E08 T7A RPCI-11 Human Male BAC Library Homo sapiens
 DEFINITION genomic clone Plate=631 Col=16 Row=J, genomic survey sequence.

ACCESSION AQ407920
 VERSION AQ407920.1 GI:4427459
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 1 (bases 1 to 534)
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
 Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 JOURNAL MEDLINE 99380589
 PUBMED 10449764
 COMMENT Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.bufileo.edu). Clones may be purchased from BACpac Resources (http://bacpac.med.bufileo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu
 Plate: 631 row: J column: 16
 Seq primer: 17
 Class: BAC ends
 High quality sequence stop: 534.
 Location/Qualifiers
 1..534
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=631 Col=16 Row=J"
 /sex="male"
 /clone.lib="RPCI-11 Human Male BAC library"
 /note="Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBAC3.6 vector at EcoRI sites"
 BASE COUNT 173 a 71 c 149 g 135 t 6 others
 ORIGIN
 Query Match 66.7%; Score 14; DB 28; Length 534;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 AACGTTCCGAGTCA 20
 Db 150 AACGTTCCGAGTCA 163
 RESULT 37
 AL695492/c 541 bp mRNA linear EST 21-MAR-2002
 LOCUS AL695492 NAPI Anopheles gambiae cDNA clone NAPI-P31-H-11-5, mRNA
 DEFINITION sequence.
 ACCESSION AL695492
 VERSION AL695492.1 GI:19615134
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anophelinae.
 1 (bases 1 to 541)
 Christophides,G.K., Blass,K., Zdobnov,E.M., Carmouche,R., Benes,V.

TITLE and Kafatos,F.C.
 JOURNAL Anopheles gambiae EST, European Molecular Biology Laboratory
 COMMENT Unpublished
 Contact: Christophides GK
 Focis C. Kafatos Laboratory
 European Molecular Biology Laboratory
 Meyerhofstrasse 1, 69117 Heidelberg, Germany
 Tel: +49 6221 387-440
 Fax: +49 6221 387-306
 Email: christophe@embi-heidelberg.de
 Plate: P31 row: H column: 11.
 Location/Qualifiers
 1..541
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /db_xref="taxon:7165"
 /clone="NAPI-P31-H-11-5"
 /lab_host="E. coli DH10B"
 /clone.lib="NAPI"
 /note="Vector: pT73D-Pac (Pharmacia); Site 1: NotI; Site 2: EcoRI; ESTs sequenced from the T7 priming site that reads from the 5' end of cDNA. The NAPI is a directionally cloned and normalized, oligo-T primed cDNA library constructed from a mixture of Anopheles gambiae developmental stages according to: Bonaldo, Lennon & Soares (1996): Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
 BASE COUNT 134 a 134 c 175 g 96 t 2 others
 ORIGIN
 Query Match 66.7%; Score 14; DB 9; Length 541;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CGAAGTTCCGAGAT 18
 Db 405 CGAAGTTCCGAGAT 392
 RESULT 38
 B1511012/c 544 bp mRNA linear EST 08-APR-2002
 LOCUS B1511012 B1600042A20E05.5 Bee Brain Normalized Library, B16 Apis mellifera
 DEFINITION cDNA clone B1600042A20E05 5', mRNA sequence.
 ACCESSION B1511012
 VERSION B1511012.1 GI:15361386
 KEYWORDS EST.
 SOURCE Apis mellifera (honeybee)
 ORGANISM Apis mellifera
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea; Apidae; Apis.
 1 (bases 1 to 544)
 Whitfield,C.W., Band,M.R., Bonaldo,M.F., Kumar,C.G., Liu,L., Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.B.
 Annotated expressed sequence tags and cDNA microarrays for studies of brain and behavior in the honey bee
 Genome Res. 12 (4), 555-566 (2002)
 JOURNAL 21929762
 MEDLINE 11932240
 PUBMED 11932240
 COMMENT Contact: Gene E. Robinson
 Department of Entomology
 University of Illinois
 505 S. Goodwin Ave., Urbana, IL 61801, USA
 Tel: 217 265 0309
 Fax: 217 244 3499
 Email: gene@life.uiuc.edu
 This research was funded by the University of Illinois Critical Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation Award in Functional Genomics to G.E. Robinson and an NSF Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
 PCR Primers

FORWARD: TAATACGACTCATAATAGG
 BACKWARD: ATTAACTCTACTAAG
 Plate: BB160004A20 row: E column: 05
 Seq primer: AGCGATACAACTTTCACACAGA
 High quality sequence stop: 544.
 Location/Qualifiers

FEATURES
 source
 1..544
 /organism="Apis mellifera"
 /mol_type="mRNA"
 /strain="mixed strains of European bees, predominantly
 A.m. ligustica"
 /db_xref="taxon:7460"
 /clone="BB160004A20E05"
 /sex="female"
 /tissue_type="brain"
 /dev_stage="adult worker honey bee"
 /lab_host="DH10B"
 /clone_lib="Bee Brain Normalized Library, BB16"
 /note="Organ: brain; Vector: pRTT3-Pac; Site 1: EcorI;
 Site 2: NotI; The BB16 library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996), Genome Research 6 (9): 791-806. RNA was
 prepared from dissected brains of adult worker bees of
 various ages and various behavioral groups. "
 BASE COUNT 119 a 147 c 143 g 135 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 544;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CGTCGACGCTTGA 15
 |||||
 Db 132 CGTCGACGCTTGA 119

RESULT 39
 BM649585/c 546 bp mRNA linear EST 26-FEB-2002
 LOCUS 17000687369108 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 DEFINITION 19600449617798 5', mRNA sequence.
 ACCESSION BM649585
 VERSION BM649585.1 GI:18949096
 KEYWORDS EST
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.
 1 (bases 1 to 546)
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
 R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 Celera Anopheles gambiae EST project
 Unpublished
 Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004N8E row: H column: 20
 Seq primer: M13 Reverse.
 Location/Qualifiers

FEATURES
 source
 1..546
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced suscep. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449617798"
 /dev_stage="Adult"
 /lab_host="DH10B"

/clone_lib="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.
 cDNA inserts >500 bp cloned directionally into pSport 1.
 Not 1 site is 3'. Clones available through the Malaria
 Research and Reference Reagent Resource Center
 (www.malaria.mr4.org)."
 BASE COUNT 132 a 145 c 176 g 93 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 546;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGCTTCGAGAT 18
 |||||
 Db 409 CGACGCTTCGAGAT 396

RESULT 40
 BM650226/c 549 bp mRNA linear EST 26-FEB-2002
 LOCUS 17000687370552 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 DEFINITION 19600449640068 5', mRNA sequence.
 ACCESSION BM650226
 VERSION BM650226.1 GI:18949737
 KEYWORDS EST
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.
 1 (bases 1 to 549)
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
 R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 Celera Anopheles gambiae EST project
 Unpublished
 Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltRA@celera.com
 Plate: NU01004AY4 row: H column: 18
 Seq primer: M13 Reverse.
 Location/Qualifiers

FEATURES
 source
 1..549
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced suscep. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449640068"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /clone_lib="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.
 cDNA inserts >500 bp cloned directionally into pSport 1.
 Not 1 site is 3'. Clones available through the Malaria
 Research and Reference Reagent Resource Center
 (www.malaria.mr4.org)."

BASE COUNT 126 a 159 c 183 g 81 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 549;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGCTTCGAGAT 18
 |||||
 Db 286 CGACGCTTCGAGAT 273

RESULT 41
BM626834 550 bp mRNA linear EST 26-FEB-2002
LOCUS BM626834/c
DEFINITION 17000687496213 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449642604 5', mRNA sequence.
ACCESSION BM626834
VERSION BM626834.1 GI:18926345
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 550)
AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
JOURNAL Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRa@celera.com
Plate: NU01003CY3 row: B column: 10
Seq primer: M13 Reverse.
Location/Qualifiers
1..550
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449642604"
/dev_stage="Adult"
/lab_host="DHI0b"
/clone_1lb="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT 131 a 151 c 187 g 81 t
ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 550;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGAAGCTTCGAGAT 18
|||||
Db 302 CGAAGCTTCGAGAT 289

RESULT 42
BM633500 554 bp mRNA linear EST 26-FEB-2002
LOCUS BM633500/c
DEFINITION 17000687507362 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449648215 5', mRNA sequence.
ACCESSION BM633500
VERSION BM633500.1 GI:18933011
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 554)
AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
JOURNAL Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRa@celera.com
Plate: NU010049W5 row: L column: 05
Seq primer: M13 Reverse.
Location/Qualifiers
1..554
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449648215"
/dev_stage="Adult"
/lab_host="DHI0b"
/clone_1lb="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT 129 a 154 c 176 g 95 t
ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 554;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGAAGCTTCGAGAT 18
|||||
Db 450 CGAAGCTTCGAGAT 437

RESULT 43
BH899413 556 bp DNA linear GSS 30-AUG-2002
LOCUS BH899413/c
DEFINITION Ots600480 Ostreococcus tauri genomic shotgun library Ostreococcus
tauri genomic clone otd60509.b 5', genomic survey sequence.
ACCESSION BH899413
VERSION BH899413.1 GI:22550908
KEYWORDS GSS.
SOURCE Ostreococcus tauri
ORGANISM Ostreococcus tauri
Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales;
Mamiellaceae; Ostreococcus.
REFERENCE 1 (bases 1 to 556)
AUTHORS Derelle, E., Ferraz, C., Lagoda, P., Eychenne, S., Cooke, R., Regad, F.,
Sabau, X., Courties, C., Delseny, M., Demallie, J., Picard, A. and
Moreau, H.
DNA libraries for sequencing the genome of Ostreococcus tauri
(Chlorophytae, Prasinophyceae): the smallest free-living eukaryotic
cell
JOURNAL J. Phycol. 38 (6), 1150-1156 (2002)
COMMENT Contact: Moreau H
Laboratoire Arago
CNRS UMR 7628
BP 44, Avenue Fontvieille, 66651 Banyuls sur mer, France
Tel: (33)468887309
Fax: (33)468887398
Email: h.moreau@obs-banyuls.fr
Seq primer: forward
Class: shotgun.
Location/Qualifiers
1..556
/organism="Ostreococcus tauri"
/mol_type="genomic DNA"
/strain="Otd60595"
/db_xref="taxon:70448"

JOURNAL Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRa@celera.com
Plate: NU010049W5 row: L column: 05
Seq primer: M13 Reverse.
Location/Qualifiers
1..554
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449648215"
/dev_stage="Adult"
/lab_host="DHI0b"
/clone_1lb="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT 129 a 154 c 176 g 95 t
ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 554;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGAAGCTTCGAGAT 18
|||||
Db 450 CGAAGCTTCGAGAT 437

RESULT 43
BH899413 556 bp DNA linear GSS 30-AUG-2002
LOCUS BH899413/c
DEFINITION Ots600480 Ostreococcus tauri genomic shotgun library Ostreococcus
tauri genomic clone otd60509.b 5', genomic survey sequence.
ACCESSION BH899413
VERSION BH899413.1 GI:22550908
KEYWORDS GSS.
SOURCE Ostreococcus tauri
ORGANISM Ostreococcus tauri
Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales;
Mamiellaceae; Ostreococcus.
REFERENCE 1 (bases 1 to 556)
AUTHORS Derelle, E., Ferraz, C., Lagoda, P., Eychenne, S., Cooke, R., Regad, F.,
Sabau, X., Courties, C., Delseny, M., Demallie, J., Picard, A. and
Moreau, H.
DNA libraries for sequencing the genome of Ostreococcus tauri
(Chlorophytae, Prasinophyceae): the smallest free-living eukaryotic
cell
JOURNAL J. Phycol. 38 (6), 1150-1156 (2002)
COMMENT Contact: Moreau H
Laboratoire Arago
CNRS UMR 7628
BP 44, Avenue Fontvieille, 66651 Banyuls sur mer, France
Tel: (33)468887309
Fax: (33)468887398
Email: h.moreau@obs-banyuls.fr
Seq primer: forward
Class: shotgun.
Location/Qualifiers
1..556
/organism="Ostreococcus tauri"
/mol_type="genomic DNA"
/strain="Otd60595"
/db_xref="taxon:70448"

/clone="otdb06b09.b"
 /note="Vector: Bluescript; Site 1: EcoRV; Site 2: EcoRV;
 Shotgun library prepared after sonication of the genomic
 DNA. Blunt ligation in EcoRV site of Bluescript. Size
 selection of the inserts after agarose electrophoresis
 between 1 and 3 Kb."
 BASE COUNT 129 a 142 c 174 g 111 t
 ORIGIN

Query Match 66.7%; Score 14; DB 28; Length 556;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTTCG 14
 |||||
 254 TCGTGAACGTTTCG 241

RESULT 44
 AZ216899 558 bp DNA linear GSS 09-JUN-2000
 DEFINITION Sheared DNA-85E2.TF Sheared DNA Trypanosoma brucei genomic clone
 Sheared DNA-85E2, genomic survey sequence.
 ACCESSION AZ216899
 VERSION AZ216899.1 GI:8434699
 KEYWORDS GSS
 SOURCE Trypanosoma brucei
 ORGANISM Trypanosoma brucei
 Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae;
 Trypanosoma.
 1 (bases 1 to 558)
 El-Sayed,N., Zhao,S., Zhao,H., Gill,S., Suh,E., Malek,J., Fujii,C.,
 Gerrard,C., Leech,V., de Jong,P., Ullu,E., Melville,S., Donelson,J.,
 Frazer,C. and Adams,M.
 Determination of clone end sequences from Trypanosoma brucei GUTat
 10.1 sheared DNA library
 Unpublished
 Other_GSS: Sheared DNA-85E2.TF
 Contact: Najib M. El-Sayed
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: nelsayed@tigr.org
 Clones are derived from the Trypanosoma brucei GUTat 10.1 sheared
 DNA library constructed at TIGR. Clones will be available for
 distribution through Research Genetics, Alabama, USA. Sheared DNA
 end sequences search page: <http://www.tigr.org/cdb/mdb/tbdb/>.
 Seq primer: M13-Forward
 Class: shotgun.

FEATURES
 source
 1..558
 Location/Qualifiers

/organism="Trypanosoma brucei"
 /mol_type="genomic DNA"
 /strain="TREU927/4 GUTat 10.1"
 /db_xref="taxon:5691"
 /clone="Sheared DNA-85E2"
 /clone_lib="Sheared DNA"

/note="Vector: pUC18; Site 1: SmaI; Constructed at The
 Institute for Genomic Research (TIGR), Rockville, MD.
 Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically
 sheared to give a tight size distribution (approx 2 kb).
 The v + i method used for the library construction is
 described in detail in Smith, H.O. and Venter, J.C.
 (Making small insert libraries for whole genome shotgun
 sequencing projects. In Genome Sequencing: A Practical
 Approach, eds. M. Vaudin and B. Barrell, Oxford University
 Press, 1999)."
 BASE COUNT 117 a 192 c 106 g 143 t
 ORIGIN

Query Match 66.7%; Score 14; DB 28; Length 558;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTGAACGTTTCG 14
 |||||
 Db 209 TCGTGAACGTTTCG 222

RESULT 45
 BM632387 561 bp mRNA linear EST 26-FEB-2002
 LOCUS BM632387
 DEFINITION 17000687504190 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 19600449668153 5', mRNA sequence.
 ACCESSION BM632387
 VERSION BM632387.1 GI:18931898
 KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.

REFERENCE 1 (bases 1 to 561)
 Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
 R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 Celera Genomics
 Celera Anopheles gambiae EST project
 Unpublished
 CONTACT: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404531151
 Fax: 2404534580
 Email: Holt@celera.com
 Plate: NU01004ABH row: J column: 23
 Seq primer: M13 Reverse.

FEATURES
 source
 1..561
 Location/Qualifiers

/organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449668153"
 /dev_stage="Adult"
 /lab_host="DHI0b"
 /clone_lib="A.Gam.ad.cDNA1"

/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.
 cDNA inserts >500 bp cloned directionally into pSport 1.
 Not I site is 3'. Clones available through the Malaria
 Research and Reference Reagent Resource Center
 (www.malaria.mr4.org)."
 BASE COUNT 131 a 148 c 187 g 95 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 561;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAAGCTCGAGAT 18
 |||||
 Db 414 CGAAGCTCGAGAT 401

RESULT 46
 BM600003 562 bp mRNA linear EST 25-FEB-2002
 LOCUS BM600003
 DEFINITION 17000687050748 A.Gam.ad.cDNA.bloodi Anopheles gambiae cDNA clone
 1960044975768 5', mRNA sequence.
 ACCESSION BM600003
 VERSION BM600003.1 GI:18898107
 KEYWORDS EST.

SOURCE	Anopheles gambiae (African malaria mosquito)			
ORGANISM	Anopheles gambiae Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.			
REFERENCE	1 (bases 1 to 562)			
AUTHORS	Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab R., Collins,F.H., Venter,J.C. and Hoffman,S.L.			
TITLE	Celera Anopheles gambiae EST project			
JOURNAL	Unpublished			
COMMENT	Contact: Holt R.A. Celera Genomics 45 W. Gude Dr., Rockville, MD 20850, USA Tel: 2404533151 Fax: 2404534580 Email: HoltRA@celera.com Plate: NT01004AYL row: K column: 02 Seq primer: M13 Reverse.			
FEATURES	Location/Qualifiers			
Source	1..562			
	/organism="Anopheles gambiae"			
	/mol_type="mRNA"			
	/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"			
	/db_xref="taxon:7165"			
	/clone="19600449725768"			
	/dev_stage="Adult"			
	/lab_host="DH10b"			
	/clone_1ib="A.Gam.ad.cDNA.blood1"			
	/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex)_frozen on liquid nitrogen 24 hours after human blood feeding. cDNA inserts >500 bp cloned directionally into pSport 1. Not I site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)"			
BASE COUNT	132 a	153 c	183 g	94 t
ORIGIN				
Query Match	66.7%;	Score 14;	DB 12;	Length 562;
Best Local Similarity	100.0%;	Pred. No. 3.2e+02;		
Matches 14;	Conservative	0;	Mismatches	0;
Indels	0;	Gaps	0;	
Cy	5	CGAAGCTTCGAGAT	18	
Db	408	CGAAGCTTCGAGAT	395	
RESULT 47				
BM621639/c				
LOCUS	BM621639	569 bp	mRNA	linear
DEFINITION	17000667447524 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone			
ACCESSION	19600449637012 5', mRNA sequence.			
VERSION	BM621639			
KEYWORDS	EST.			
SOURCE	BM621639.1 GI:18920057			
ORGANISM	Anopheles gambiae (African malaria mosquito)			
	Anopheles gambiae			
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.			
REFERENCE	1 (bases 1 to 569)			
AUTHORS	Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab R., Collins,F.H., Venter,J.C. and Hoffman,S.L.			
TITLE	Celera Anopheles gambiae EST project			
JOURNAL	Unpublished			
COMMENT	Contact: Holt R.A. Celera Genomics 45 W. Gude Dr., Rockville, MD 20850, USA Tel: 2404533151 Fax: 2404534580 Email: HoltRA@celera.com Plate: NT01004AYL row: I column: 10 Seq primer: M13 Reverse.			

FEATURES	Location/Qualifiers
SOURCE	1..569
	/organism="Anopheles gambiae"
	/mol_type="mRNA"
	/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
	/db_xref="taxon:7165"
	/clone="19600449637012"
	/dev_stage="Adult"
	/lab_host="DH10b"
	/clone_1b="A.Gam.ad.cDNA1"
	/note="Vector: pSport1; Site_1: SalI; Site_2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
BASE COUNT	135 a 151 c 187 g 96 t
ORIGIN	
Query Match	66.7%; Score 14; DB 12; Length 569;
Best Local Similarity	100.0%; Pctd. No. 3..2e+02;
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
cy	5 CGACGTTCCAGAT 18
Db	430 CGACGTTCCAGAT 417
RESULT 48	
BM619639/c	571 bp mRNA linear EST 25-FEB-2002
LOCUS	17000687440685 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION	19600449657860 5', mRNA sequence.
ACCESSION	BM619639
VERSION	BM619639.1
KEYWORDS	GI:18918057
SOURCE	EST.
ORGANISM	Anopheles gambiae (African malaria mosquito)
	Anopheles gambiae
	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
	Anophelinae.
REFERENCE	1 (bases 1 to 571)
AUTHORS	Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
TITLE	,R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
JOURNAL	Celera Anopheles gambiae EST project
COMMENT	Unpublished
	Contact: Holt R.A.
	Celera Genomics
	45 W. Gude Dr., Rockville, MD 20850, USA
	Tel.: 2404533151
	Fax: 2404534580
	Email: HoltRA@celera.com
	Plate: NU01004AB6 row: N column: 02
	Seq primer: M13 Reverse.
FEATURES	Location/Qualifiers
SOURCE	1..571
	/organism="Anopheles gambiae"
	/mol_type="mRNA"
	/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
	/db_xref="taxon:7165"
	/clone="19600449657860"
	/dev_stage="Adult"
	/lab_host="DH10b"
	/clone_1b="A.Gam.ad.cDNA1"
	/note="Vector: pSport1; Site_1: SalI; Site_2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
BASE COUNT	142 a 151 c 188 g 90 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 571;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18
 |||||
 118 CGAAGCTTCGAGAT 105

Db

RESULT 49
 BM645614/c 572 bp mRNA linear EST 26-FEB-2002
 LOCUS 17000687316797 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 DEFINITION 1960049663794 5', mRNA sequence.
 ACCESSION BM645614
 VERSION BM645614.1 GI:18945125
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 1 (bases 1 to 572)
 Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 Celera Anopheles gambiae EST project
 Unpublished
 Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltR@celera.com
 Plate: NU01004187 row: E column: 08
 Seq primer: M13 Reverse.
 Location/Qualifiers

FEATURES
 source 1..572
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
 /db_xref="taxon:7165"
 /clone="1960049663794"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cDNA1"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSPORT 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
 BASE COUNT 137 a 151 c 188 g 96 t
 ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 572;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTCGAGAT 18
 |||||
 400 CGAAGCTTCGAGAT 387

Db

RESULT 50
 AI667035 577 bp mRNA linear EST 07-JUN-2001
 LOCUS FC24912.y1 Zebrafish Mashu MP1MG EST Danio rerio cDNA clone
 DEFINITION IMAGE:3722374 5', mRNA sequence.
 ACCESSION AI667035
 VERSION AI667035.1 GI:4805391

KEYWORDS EST.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 577)
 Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Bady, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Szegete, M., Theising, B., Allen, M., Bowers, Y., Peterson, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Rletter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
 Mashu Zebrafish EST Project 1998
 Unpublished
 Contact: Stephen L. Johnson
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: zbrfish@wustl.edu
 cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and ResourcenZentrumPrimaDatenbank, Berlin, Germany (web address: www.rzpd.de)
 Seq primer: T3 ET from Amersham
 High quality sequence stop: 481.
 Location/Qualifiers

FEATURES
 source 1..577
 /organism="Danio rerio"
 /mol_type="mRNA"
 /db_xref="taxon:7955"
 /clone="IMAGE:3722374"
 /sex="mixed"
 /tissue_type="26 somite embryos, adult livers, shield stage embryos"
 /lab_host="Xla-blue MRF"
 /clone_lib="Zebrafish Mashu MP1MG EST"
 /note="Vector: pSPORT1; Site 1: NotI; Site 2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer (5' PGACTAGTCTTAGATCGGACGCGCCCTTTTCTTTT3'), double-stranded cDNA was ligated into Sal I adaptor (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."
 BASE COUNT 140 a 126 c 154 g 157 t
 ORIGIN

Query Match 66.7%; Score 14; DB 9; Length 577;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACGTTGAGATGA 20
 |||||
 406 AACGTTGAGATGA 419

Db

RESULT 51

BM650798/c 578 bp mRNA linear EST 26-FEB-2002

LOCUS BM650798 578 bp mRNA linear EST 26-FEB-2002

DEFINITION 1700068732563 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone

ACCESSION 1960049637545 5', mRNA sequence.

BM650798

VERSION BM650798.1 GI:18950309

KEYWORDS EST.

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.

REFERENCE 1 (bases 1 to 578)

AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab

TITLE R., Collins,F.H., Venter,U.C. and Hoffman,S.L.

JOURNAL Celera Anopheles gambiae EST project

COMMENT Unpublished

Contact: Holt R.A.

Celera Genomics

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NU01004AYT row: O column: 15

Seq primer: M13 Reverse

FEATURES

source

1..578

Location/Qualifiers

/organism="Anopheles gambiae"

/mol_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"

/db_xref="taxon:7165"

/clone="1960049637545"

/dev_stage="Adult"

/lab_host="DH10b"

/clone_lib="A.Gam.ad.cDNA1"

/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.war.org)."

BASE COUNT 138 a 154 c 185 g 101 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 578;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 CGAAGCTTCGAGAT 18

|||||

Db 426 CGAAGCTTCGAGAT 413

RESULT 52

BM279238 582 bp mRNA linear EST 20-DEC-2001

LOCUS BM279238 582 bp mRNA linear EST 20-DEC-2001

DEFINITION Nb ad1 04E02 M13 Nipostromylius brasiliensis uni-zap adult library

Nipostromylius brasiliensis cDNA clone Nb ad1 04E02 5' similar to ref|NP_492164.1| (NM_059763) PZ2 domain (Also known as DHR or GUGP).

Accession: BM279238.1 GI:17972496

VERSION BM279238

KEYWORDS EST.

SOURCE Nipostromylius brasiliensis

ORGANISM Nipostromylius brasiliensis

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongyloida; Trichostrongyloidea; Heligmonellidae; Nipostromylinae; Nipostromylinus.

REFERENCE 1 (bases 1 to 582)

AUTHORS Harcus,Y. and Matzeis,R.M.

TITLE Sequence survey of Nipostromylius brasiliensis

JOURNAL Unpublished

COMMENT Contact: Matzeis RM

Institute of Cell, Animal and Population Biology

University of Edinburgh

Ashworth Labs, West Mains Road, Edinburgh EH93JT, Scotland

Tel: +44 131 650 5511

Fax: +44 131 650 5450

Email: r.matzeis@ed.ac.uk

The library was prepared by Murray Selkirk, Imperial College, London. Sequencing was performed by Yvonne Harcus, Edinburgh University, UK

PCR Primers

FORWARD: T3

BACKWARD: T7PL

Plate: 04 row: B column: 02

Seq primer: M13

High quality sequence stop: 582.

FEATURES

source

1..582

Location/Qualifiers

/organism="Nipostromylius brasiliensis"

/mol_type="mRNA"

/db_xref="taxon:27835"

/clone="Nb ad1 04E02"

/dev_stage="adult"

/clone_lib="Nipostromylius brasiliensis uni-zap adult library"

/note="Vector: pBluescript SK+; The library was prepared in Murray Selkirk's lab, Imperial College, London."

BASE COUNT 159 a 135 c 143 g 145 t

ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 582;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 ACGTTCGAGATGAT 21

|||||

Db 212 ACGTTCGAGATGAT 225

RESULT 53

BF157792 583 bp mRNA linear EST 23-FEB-2001

LOCUS BF157792 583 bp mRNA linear EST 23-FEB-2001

DEFINITION BF144966.y1 Sugano Kawakami zebrafish DNA Danio rerio cDNA clone

IMAGE:3816778 5', mRNA sequence.

ACCESSION BF157792

VERSION BF157792.1 GI:11052991

KEYWORDS EST.

SOURCE Danio rerio (zebrafish)

ORGANISM Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

REFERENCE 1 (bases 1 to 583)

AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Rddy

S., Hillier,L., Kucaba,T., Martin,D., Beck,C., Wiley,T., Underwood

K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Page,D., Harvey,N., Schurk,R., Rittler,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.

TITLE Maenu zebrafish EST Project 1998

JOURNAL Unpublished

COMMENT Contact: Stephen L. Johnson

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrafish@wustl.edu

Library constructed by Dr. Sumio Sugano and Dr. Koichi Kawakami DNA Sequencing by: Washington University Genome Sequencing Center Clome distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to: info@image.lnl.gov

Seq primer: T3 Et from Amersham

High quality sequence stop: 514.


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FEATURES
source
    Location/Qualifiers
    1..583
    /organism="Pantio xerlio"
    /mol_type="mRNA"
    /strain="AB"
    /db_xref="taxon:7955"
    /clone="IMAGE:3816778"
    /sex="mixed (one male and one female, including
    unfertilized eggs)"
    /dev_stage="adult"
    /lab_host="DH10b (phage resistant)"
    /clone_lib="Sugano Kawakami zebrafish DR1"
    /note="Vector: pME18s-FL3; Site 1: DraIII (CACTGTCG);
    Site 2: DraIII (CACCAGTCG); 1st strand cDNA was primed
    with an oligo(dT) primer [ATGTGGCCCTTTTCTTTTCTTTT];
    double-stranded cDNA was ligated to a DraIII adaptor
    (TGTGGCCCTCTG), digested and cloned into distinct DraIII
    sites of the pME18s-FL3 vector (5' site CACTGTCG, 3' site
    CACCAGTCG). XhoI should be used to isolate the cDNA
    insert. Size selection was performed to exclude fragments
    <1.5kb. Library constructed by Dr. Sumio Sugano
    (University of Tokyo Institute of Medical Science) and
    kindly donated by Dr. Koichi Kawakami. Custom primers for
    sequencing: 5' end primer CTCTGCTCTAAAGCTGCG and 3' end
    primer CGACCTCGACGCTCGACACA."
BASE COUNT    139 a    148 c    152 g    143 t    1 others
ORIGIN

Query Match    66.7%; Score 14; DB 10; Length 583;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
Db    7 AACGTTCCGAGATCA 20
      |||||
      261 AACGTTCCGAGATCA 274

RESULT 54
BM630963/c    588 bp    mRNA    linear    EST 26-FEB-2002
LOCUS
DEFINITION
17000687502159 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449617012 5', mRNA sequence.
ACCESSION
BM630963
VERSION
BM630963.1 GI:18930474
KEYWORDS
EST
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 588)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU0100496A row: H column: 02
Seq primer: M13 Reverse
Location/Qualifiers
1..588
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced suc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449617012"
/dev_stage="Adult"
/lab_host="DH10b"

FEATURES
source
    Location/Qualifiers
    1..588
    /organism="Anopheles gambiae"
    /mol_type="mRNA"
    /strain="RSP-ST (Reduced suc. to Permethrin - std.
    chromosome)"
    /db_xref="taxon:7165"
    /clone="19600449617012"
    /dev_stage="Adult"
    /lab_host="DH10b"

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```

/clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT    143 a    160 c    191 g    94 t
ORIGIN

Query Match    66.7%; Score 14; DB 12; Length 588;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
Db    5 CGAAGTTCCGAGAT 18
      |||||
      109 CGAAGTTCCGAGAT 96

RESULT 55
BM649878/c    592 bp    mRNA    linear    EST 26-FEB-2002
LOCUS
DEFINITION
17000687369980 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449651232 5', mRNA sequence.
ACCESSION
BM649878
VERSION
BM649878.1 GI:18949389
KEYWORDS
EST
SOURCE
Anopheles gambiae (African malaria mosquito)
ORGANISM
Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 592)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU0100496C row: I column: 22
Seq primer: M13 Reverse
Location/Qualifiers
1..592
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced suc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449651232"
/dev_stage="Adult"
/lab_host="DH10b"
/clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT    138 a    158 c    199 g    97 t
ORIGIN

Query Match    66.7%; Score 14; DB 12; Length 592;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
Db    5 CGAAGTTCCGAGAT 18
      |||||
      442 CGAAGTTCCGAGAT 429

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RESULT 56
BM624679/c 593 bp mRNA linear EST 26-FEB-2002
LOCUS 1700068749166 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION 19600449643241 5', mRNA sequence.
ACCESSION BM624679
VERSION BM624679.1 GI:18924190
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 593)
AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celeris Anopheles gambiae EST project
JOURNAL Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@celera.com
Plate: NU01004AY9 row: L column: 23
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source 1..593
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449643241"
/dev_stage="Adult"
/lab_host="DHI0b"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT 140 a 155 c 184 g 114 t
ORIGIN
Query Match 66.7%; Score 14; DB 12; Length 593;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTCGAGAT 18
|||||
Db 459 CGACGTCGAGAT 446

RESULT 57
BM622534/c 595 bp mRNA linear EST 26-FEB-2002
LOCUS 17000687476438 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION 19600449643086 5', mRNA sequence.
ACCESSION BM622534
VERSION BM622534.1 GI:18922045
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 595)
AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celeris Anopheles gambiae EST project
JOURNAL Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@celera.com
Plate: NU01004NBW row: E column: 16
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source 1..595
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449625402"
/dev_stage="Adult"

JOURNAL Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@celera.com
Plate: NU01004AY9 row: F column: 12
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source 1..595
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449643086"
/dev_stage="Adult"
/lab_host="DHI0b"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT 142 a 156 c 194 g 103 t
ORIGIN
Query Match 66.7%; Score 14; DB 12; Length 595;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTCGAGAT 18
|||||
Db 426 CGACGTCGAGAT 413

RESULT 58
BM632552/c 595 bp mRNA linear EST 26-FEB-2002
LOCUS 17000687504447 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION 19600449625402 5', mRNA sequence.
ACCESSION BM632552
VERSION BM632552.1 GI:18932063
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
REFERENCE 1 (bases 1 to 595)
AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celeris Anopheles gambiae EST project
JOURNAL Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltR@celera.com
Plate: NU01004NBW row: E column: 16
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source 1..595
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449625402"
/dev_stage="Adult"

Query Match	Score 14;	DB 12;	Length 595;
Best Local Similarity	100.0%;	Pred. No. 3.2e+02;	
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0
BASE COUNT	148 a	158 c	157 g 92 t
ORIGIN			
Query Match	66.7%;	Score 14;	DB 12;
Best Local Similarity	100.0%;	Pred. No. 3.2e+02;	
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0
BASE COUNT	144 a	158 c	194 g 104 t
ORIGIN			
Query Match	66.7%;	Score 14;	DB 12;
Best Local Similarity	100.0%;	Pred. No. 3.2e+02;	
Matches 14;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0
BASE COUNT	144 a	158 c	194 g 104 t
ORIGIN			

[illegible]

SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 REFERENCE 1 (bases 1 to 606)
 AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 TITLE Celera Anopheles gambiae EST project
 JOURNAL Unpublished
 COMMENT Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltR@celera.com
 Plate: NU01004AYL row: C column: 07
 Seq primer: M13 Reverse
 Location/Qualifiers
 1..606
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449636865"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cDNA1"
 /note="Vector: pSPori; Site_1: SalI; Site_2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSPori 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.m4.org)."
 BASE COUNT 155 a 162 c 201 g 88 t
 ORIGIN
 Query Match 66.7%; Score 14; DB 12; Length 606;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CGAAGCTTCGAGAT 18
 |||||
 |||||
 Db 336 CGAAGCTTCGAGAT 323
 RESULT 62
 BH416973 606 bp DNA linear GSS 12-DEC-2001
 LOCUS 1007052A03.xl 1007 - Rescuedu Grid H Zea mays genomic, genomic
 DEFINITION survey sequence.
 ACCESSION BH416973
 VERSION BH416973.1 GI:17600729
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 606)
 Walbot, V.
 Maize genomic sequences found using engineered Rescuedu transposon
 JOURNAL Unpublished
 COMMENT Contact: Walbot V
 Department of Biological Sciences
 Stanford University
 855 California Ave, Palo Alto, CA 94304, USA
 Tel: 650 723 2227
 Fax: 650 725 8221
 Email: walbot@stanford.edu
 Plate: 1007052 column: 30
 Class: transposon-tagged.

FEATURES
 source Location/Qualifiers
 1..606
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /cultivar="mixed background W23/A188/B73"
 /db_xref="taxon:4577"
 /tissue_type="leaf"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="1007 - Rescuedu Grid H"
 /note="Organ: leaf; Vector: Rescuedu (engineered from pBluescript backbone); Site_1: BamHI; Site_2: BglII; Rescuedu is a 4.9 Kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuedu, go to the web site 'www.zmmb.iastate.edu' and follow the links for 'Rescuedu'. Grid H was grown at Berkeley in 2001. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."
 BASE COUNT 143 a 141 c 146 g 174 t 2 others
 ORIGIN
 Query Match 66.7%; Score 14; DB 28; Length 606;
 Best Local Similarity 100.0%; Pred. No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 CGAAGCTTCGAGAT 18
 |||||
 |||||
 Db 434 CGAAGCTTCGAGAT 421
 RESULT 63
 BM634523 614 bp mRNA linear EST 26-FEB-2002
 LOCUS 17000687509206 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 DEFINITION 19600449654085 5', mRNA sequence.
 ACCESSION BM634523
 VERSION BM634523.1 GI:18934034
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
 REFERENCE 1 (bases 1 to 614)
 AUTHORS Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
 TITLE Celera Anopheles gambiae EST project
 JOURNAL Unpublished
 COMMENT Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltR@celera.com
 Plate: NU01004AYN row: P column: 19
 Seq primer: M13 Reverse
 Location/Qualifiers
 1..614
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449654085"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cDNA1"
 /note="Vector: pSPori; Site_1: SalI; Site_2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen."

CDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mt4.org)."

BASE COUNT 153 a 164 c 202 g 95 t

Query Match 66.7%; Score 14; DB 12; Length 614;

Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTTGAGAT 18
|||||
364 CGACGTTGAGAT 351

RESULT 64 BM625508 616 bp mRNA linear EST 26-FEB-2002
LOCUS BM625508/c 17000687493212 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION 19600449662124 5', mRNA sequence.

ACCESSION BM625508
VERSION BM625508.1 GI:18925019
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.

REFERENCE 1 (bases 1 to 616)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project

TITLE Celera Anopheles gambiae EST project
JOURNAL Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404531351
Fax: 2404534580
Email: HoltR@celera.com
Plate: NU0100418B row: O column: 18
Seq primer: M13 Reverse.

FEATURES
source 1..616
Location/Qualifiers
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449662124"
/dev_stage="Adult"
/lab_host="DHI0B"
/clone_1lb="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mt4.org)."

BASE COUNT 156 a 163 c 196 g 101 t

Query Match 66.7%; Score 14; DB 12; Length 616;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGACGTTGAGAT 18
|||||
34 CGACGTTGAGAT 21

RESULT 65
AQ880074/c

LOCUS AQ880074 617 bp DNA linear GSS 09-NOV-1999
DEFINITION HS 4867_A1 E01 77A CIT Approved Human Genomic Sperm Library D Homo
sequence. genomic clone Plate=4867 Col=1 Row=1, genomic survey
sequence.

ACCESSION AQ880074 GI:6311541

VERSION AQ880074
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 617)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

TITLE High Throughput Sequencing Center
JOURNAL High Throughput Sequencing Center
MEDLINE 99380589
PUBMED 10449764
COMMENT Contract: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones have been purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 4867 row: I column: 1
Seq primer: T7
Class: BAC ends
High quality sequence stop: 617.

FEATURES
source 1..617
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=4867 Col=1 Row=I"
/sex="male"
/clone_1lb="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"

BASE COUNT 174 a 165 c 118 g 153 t 7 others

Query Match 66.7%; Score 14; DB 28; Length 617;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ACCTTCGAGATCAT 21
|||||
510 ACCTTCGAGATCAT 497

RESULT 66 BM591817 619 bp mRNA linear EST 25-FEB-2002
LOCUS BM591817/c 170006874935900 A.Gam.ad.cDNA.D1001 Anopheles gambiae cDNA clone
DEFINITION 19600449730335 5', mRNA sequence.

ACCESSION BM591817
VERSION BM591817.1 GI:18887678
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.

REFERENCE 1 (bases 1 to 619)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab
R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
JOURNAL Unpublished

COMMENT

Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 240453151
Fax: 2404534580
Email: HoltR@celera.com
Plate: NU010049UV row: 1 column: 09
Seq primer: M13 Reverse.
Location/Qualifiers

FEATURES

source

1..619

/organism="Anopheles gambiae"

/mol_type="mRNA"

/strain="RSP-ST (reduced susc. to permethrin - std.

chromosome)"

/db_xref="taxon:7165"

/dev_stage="Adult"

/lab_host="DH10b"

/clone_lib="A.Gam.ad.cDNA.blood1"

/note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
hours after human blood feeding. cDNA inserts >500 bp
cloned directionally into pSport 1. Not 1 site is 3'.
Clones available through the Malaria Research and
Reference Reagent Resource Center (www.malaria.mt4.org)"

BASE COUNT
ORIGIN

146 a 160 c 199 g 114 t

Query Match

Best Local Similarity 100.0%; Pred.No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGACGTTTCG 14
|||||

Db 257 TCGTCGACGTTTCG 244

RESULT 67
LOCUS

CC120030 627 bp DNA linear GSS 16-APR-2003

DEFINITION

NDL.76020.T7 Notre Dame Liverpool Aedes aegypti genomic clone

ACCESSION

CC120030

VERSION

CC120030.1 GI:29989085

KEYWORDS

GSS.
Aedes aegypti (yellow fever mosquito)

SOURCE

Aedes aegypti

ORGANISM

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Aedes.

REFERENCE

1 (bases 1 to 627)

AUTHORS

Loftus,B., Shetty,J., Knudson,D. and Severson,D.

TITLE

BAC end sequencing of Aedes aegypti

JOURNAL

Unpublished

COMMENT

Other GSSs: NDL.76020.SP6

CONTACT

Contact: Brendan Loftus

TI GR

Department of Eukaryotic Genomics

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: ente@tigr.org

Library was provided by David Severson

Seq primer: T7

Class: BAC ends.

Location/Qualifiers

1..627

/organism="Aedes aegypti"

/mol_type="genomic DNA"

/strain="Liverpool"

/db_xref="taxon:7159"

/clone_lib="NDL.76020"

/note="Vector: pECBAC1; Site_1: Hind III; The library was

BASE COUNT

159 a 148 c 149 g 171 t

Query Match

Best Local Similarity 100.0%; Pred.No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGACGTTTCG 14
|||||

Db 587 TCGTCGACGTTTCG 574

RESULT 68
LOCUS

AM288450 628 bp mRNA linear EST 16-JAN-2000

DEFINITION

MBTMADA198SAC Trichuris muris (parasitic nematode) mixed adult

ACCESSION

AM288450

VERSION

AM288450.1 GI:6695342

KEYWORDS

EST.

SOURCE

Trichuris muris

ORGANISM

Eukaryota; Metazoa; Nematoda; Enoplaea; Trichocephalida; Trichuridae

REFERENCE

1 (bases 1 to 628)

AUTHORS

Daub,J., Grenier,R. and Blaxter,M.

TITLE

A survey of genes expressed in adults of the whipworm Trichuris

muris

Unpublished

COMMENT

Contact: Blaxter M.

Institute of Cell, Animal and Population Biology

University of Edinburgh

Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9

3JT, UK.

Tel: +44 131 650 6760

Fax: +44 131 670 5450

Email: mark.blaxter@ed.ac.uk

The Trichuris muris EST dataset (including the TWC clustering

information) is available on the www at http://www.ed.ac.uk/ttlide

(mbx/small_genomes.html)

PCR Primers

FORWARD: M13 Reverse (AGCGATACATTTTCACACAGA)

BACKWARD: T7PL (CTCATAAGGCGCAATTGG)

Seq primer: SAC (GGGACAAAGCTGAG).

Location/Qualifiers

1..628

/organism="Trichuris muris"

/mol_type="mRNA"

/db_xref="taxon:70415"

/clone="MBTMADA198"

/sex="mixed"

/dev_stage="adult"

/clone_lib="Trichuris muris (parasitic nematode) mixed

adult"

/note="Vector: Lambda Zap II; Site_1: EcoRI (5'end);

Site_2: XhoI (3'end); Trichuris muris is a nematode

parasite of rodents related to the human whipworm

Trichuris trichiura. The library was constructed from

Trichuris muris adults (Edinburgh 'E' strain) maintained

in mice, and was provided by Dr. Richard Grenier,

University of Manchester."

BASE COUNT

166 a 170 c 91 g 201 t

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred.No. 3.2e+02;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 AACGTCGAGATGA 20
|||||

Db 363 AACGTTGAGATGA 350

RESULT 69
LOCUS BM641079 628 bp mRNA linear EST 26-FEB-2002
DEFINITION 17000687307001 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449654480 5', mRNA sequence.
BM641079
ACCESSION BM641079
VERSION BM641079.1 GI:18940590
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
1 (bases 1 to 628)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU010049WT row: N column: 04
Seq primer: M13 Reverse.
Location/Qualifiers
1..628
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449621382"
/dev_stage="Adult"
/lab_host="DH10b"
/clone_lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
BASE COUNT 153 a 163 c 208 g 104 t
ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 628;
Best Local Similarity 100.0%; Pred.No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAACGTTGAGAT 18
|||||
Db 382 CGAACGTTGAGAT 369

RESULT 70
LOCUS BM622163 629 bp mRNA linear EST 26-FEB-2002
DEFINITION 17000687475928 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449654480 5', mRNA sequence.
BM622163
ACCESSION BM622163
VERSION BM622163.1 GI:18921686
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
1 (bases 1 to 629)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab

TITLE R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
JOURNAL Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU010049WT row: A column: 06
Seq primer: M13 Reverse.
Location/Qualifiers
1..629
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
BASE COUNT 139 a 166 c 201 g 123 t
ORIGIN

Query Match 66.7%; Score 14; DB 12; Length 629;
Best Local Similarity 100.0%; Pred.No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAACGTTGAGAT 18
|||||
Db 485 CGAACGTTGAGAT 472

RESULT 71
LOCUS BM655453 629 bp mRNA linear EST 26-FEB-2002
DEFINITION 17000687386557 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
19600449627614 5', mRNA sequence.
BM655453
ACCESSION BM655453
VERSION BM655453.1 GI:18954964
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
1 (bases 1 to 629)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished
COMMENT Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 2404533151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU010049VY row: A column: 20
Seq primer: M13 Reverse.
Location/Qualifiers
1..629
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"

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/clone="19600449627614"
/dev_stage="Adult"
/lab_host="DH10b"
/clone.lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT      150 a      168 c      216 g      95 t
ORIGIN

Query Match      66.7%; Score 14; DB 12; Length 629;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGACGTTGAGAT 18
|||||
302 CGACGTTGAGAT 289

RESULT 72
BM625565/c      631 bp      mRNA      linear      EST 26-FEB-2002
LOCUS      17000687493286 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION      19600449629012 5', mRNA sequence.
ACCESSION      BM625565
VERSION      BM625565
KEYWORDS      EST
SOURCE      Anopheles gambiae (African malaria mosquito)
ORGANISM      Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 631)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 240453151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU010049W1 row: L column: 02
Seq primer: M13 Reverse
Location/Qualifiers
1. 631
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449629012"
/dev_stage="Adult"
/lab_host="DH10b"
/clone.lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT      153 a      162 c      209 g      107 t
ORIGIN

Query Match      66.7%; Score 14; DB 12; Length 631;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGACGTTGAGAT 18
|||||
302 CGACGTTGAGAT 18

```

```

|||||
Db      389 CGACGTTGAGAT 376

RESULT 73
BM654222/c      631 bp      mRNA      linear      EST 26-FEB-2002
LOCUS      17000687380327 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION      19600449631529 5', mRNA sequence.
ACCESSION      BM654222
VERSION      BM654222
KEYWORDS      EST
SOURCE      Anopheles gambiae (African malaria mosquito)
ORGANISM      Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 631)
Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
Celera Anopheles gambiae EST project
Unpublished
Contact: Holt R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 240453151
Fax: 2404534580
Email: HoltRA@celera.com
Plate: NU010049W1 row: D column: 23
Seq primer: M13 Reverse
Location/Qualifiers
1. 631
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std.
chromosome)"
/db_xref="taxon:7165"
/clone="19600449631529"
/dev_stage="Adult"
/lab_host="DH10b"
/clone.lib="A.Gam.ad.cDNA1"
/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole
adult mosquitoes (mixed sex) frozen on liquid nitrogen.
cDNA inserts >500 bp cloned directionally into pSport 1.
Not 1 site is 3'. Clones available through the Malaria
Research and Reference Reagent Resource Center
(www.malaria.mr4.org)."
BASE COUNT      152 a      162 c      207 g      110 t
ORIGIN

Query Match      66.7%; Score 14; DB 12; Length 631;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGACGTTGAGAT 18
|||||
407 CGACGTTGAGAT 394

RESULT 74
BM597192/c      633 bp      mRNA      linear      EST 25-FEB-2002
LOCUS      17000687490421 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
DEFINITION      19600449718154 5', mRNA sequence.
ACCESSION      BM597192
VERSION      BM597192
KEYWORDS      EST
SOURCE      Anopheles gambiae (African malaria mosquito)
ORGANISM      Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Anopheles.
1 (bases 1 to 633)

```


AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
 TITLE 'R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 JOURNAL Celera Anopheles gambiae EST project
 COMMENT Unpublished

Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltR@celera.com
 Plate: NU010049VS row: M column: 20
 Seq primer: M13 Reverse.

FEATURES
 source Location/Qualifiers

1..633
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"
 /db_xref="taxon:7165"
 /clone="19600449718154"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cDNA.blood1"
 /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen 24
 hours after human blood feeding. cDNA inserts >500 bp
 cloned directionally into pSport 1. Not 1 site is 3'.
 Clones available through the Malaria Research and
 Reference Reagent Resource Center (www.malaria.mr4.org)"

BASE COUNT 152 a 163 c 208 g 110 t

ORIGIN

Query Match 66.7% Score 14; DB 12; Length 633;
 Best Local Similarity 100.0%; Pred.No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAACGTTGAGAT 18
 |||||
 Db 407 CGAACGTTGAGAT 394

RESULT 75 BM636272 636 bp mRNA linear EST 26-FEB-2002
 LOCUS BM636272/c 17000668938404 A.Gam.ad.cDNA1 Anopheles gambiae cDNA clone
 DEFINITION 19600448419407 5', mRNA sequence.

ACCESSION BM636272
 VERSION BM636272.1 GI:18935783
 KEYWORDS EST.
 SOURCE Anopheles gambiae (African malaria mosquito)
 ORGANISM Anopheles gambiae
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
 Anopheles.

REFERENCE 1 (bases 1 to 636)
 AUTHORS Holt,R.A., Lin,J.-J., Murphy,S.D., Evans,C.A., Kraft,C.L., Charlab
 TITLE 'R., Collins,F.H., Venter,J.C. and Hoffman,S.L.
 JOURNAL Celera Anopheles gambiae EST project
 COMMENT Unpublished

Contact: Holt R.A.
 Celera Genomics
 45 W. Gude Dr., Rockville, MD 20850, USA
 Tel: 2404533151
 Fax: 2404534580
 Email: HoltR@celera.com
 Plate: NU01004814 row: C column: 14
 Seq primer: M13 Reverse.

FEATURES
 source Location/Qualifiers
 1..636
 /organism="Anopheles gambiae"
 /mol_type="mRNA"
 /strain="RSP-ST (Reduced susc. to Permethrin - std.
 chromosome)"

/db_xref="taxon:7165"
 /clone="19600448419407"
 /dev_stage="Adult"
 /lab_host="DH10b"
 /clone_lib="A.Gam.ad.cDNA1"
 /note="Vector: pSport1; Site_1: SalI; Site_2: NotI; Whole
 adult mosquitoes (mixed sex) frozen on liquid nitrogen.
 cDNA inserts >500 bp cloned directionally into pSport 1.
 Not 1 site is 3'. Clones available through the Malaria
 Research and Reference Reagent Resource Center
 (www.malaria.mr4.org)."

BASE COUNT 158 a 168 c 209 g 101 t

ORIGIN

Query Match 66.7% Score 14; DB 12; Length 636;
 Best Local Similarity 100.0%; Pred.No. 3.2e+02;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CGAACGTTGAGAT 18
 |||||
 Db 369 CGAACGTTGAGAT 356

Search completed: December 17, 2003, 10:00:44
 Job time : 1320 secs

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82	14	66.7	18	24	ABQ75210	ISS immunomodulat
83	14	66.7	19	24	ABQ75174	ISS immunomodulat
84	14	66.7	19	24	ABQ75175	ISS immunomodulat
85	14	66.7	20	24	ABQ75220	ISS immunomodulat
86	14	66.7	24	24	ABQ75152	ISS immunomodulat
87	14	66.7	24	24	ABQ75152	ISS immunomodulat
88	14	66.7	24	24	ABQ75152	ISS immunomodulat
89	14	66.7	24	24	ABQ75152	ISS immunomodulat
90	14	66.7	24	24	ABQ75152	ISS immunomodulat
91	14	66.7	24	24	ABQ75152	ISS immunomodulat
92	14	66.7	24	24	ABQ75152	ISS immunomodulat
93	14	66.7	24	24	ABQ75152	ISS immunomodulat
94	14	66.7	24	24	ABQ75152	ISS immunomodulat
95	14	66.7	24	24	ABQ75152	ISS immunomodulat
96	14	66.7	24	24	ABQ75152	ISS immunomodulat
97	14	66.7	24	24	ABQ75152	ISS immunomodulat
98	14	66.7	24	24	ABQ75152	ISS immunomodulat
99	14	66.7	24	24	ABQ75152	ISS immunomodulat
100	14	66.7	24	24	ABQ75152	ISS immunomodulat

ALIGNMENTS

RESULT 1
ABQ75182 standard; DNA; 21 BP.
ABQ75182;
05-NOV-2002 (first entry)
ISS immunomodulatory oligonucleotide SEQ ID NO:132.

Immunomodulatory sequence; ISS: immunomodulatory; immune response;
allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
virucide; antibacterial; protozoacide; ss.

Synthetic.
WO200252002-A2.
04-JUL-2002.
27-DEC-2001; 2001WO-US50821.
27-DEC-2000; 2000US-258675P.
(DYNA-) DYNAVAX TECHNOLOGIES CORP.
Fearon KL, Dina D;
WPI; 2002-657426/70.
Immunomodulatory polynucleotide for modulating an immune response in a
subject suffering from disorders associated with Th2-type immune
response, e.g. allergy, or infectious disease, comprises an
immunostimulatory sequence -
Claim 4; Page 21; 95pp; English.

The present invention describes an immunomodulatory polynucleotide (I)
comprising an immunostimulatory sequence (ISS). Also described: (1) an
immunomodulatory composition comprising (I); (2) an immunomodulatory
polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
biodegradable MC, where the MC is less than 10 micrometre in size; and
(3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
antibacterial and protozoacide activities, and can be used as a modulator
of immune response. (I) is useful for modulating an immune response in an
individual suffering from disorders associated with a Th2-type immune

response, especially an allergy or asthma, or an infectious disease. (I)
is also useful for increasing interferon-gamma (IFN-gamma) in an
individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
individual having a viral infection. (I) is further useful for
ameliorating a symptom of an infectious disease caused by a cellular
pathogen such as mycobacterial disease, malaria, leishmaniasis,
toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
symptom of an immunoglobulin E (IgE)-related disorder, preferably an
allergy-related disorder, in particular asthma in an individual. The
present sequence represents an immunomodulatory oligonucleotide from
the present invention.

Sequence 21 BP; 5 A; 4 C; 6 G; 6 T; 0 other;
Query Match 100.0%; Score 21; DB 24; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
ABQ75170 standard; DNA; 19 BP.
ABQ75170;
05-NOV-2002 (first entry)
ISS immunomodulatory oligonucleotide SEQ ID NO:19.

Immunostimulatory sequence; ISS: immunomodulatory; immune response;
allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
virucide; antibacterial; protozoacide; ss.

Synthetic.
WO200252002-A2.
04-JUL-2002.
27-DEC-2001; 2001WO-US50821.
27-DEC-2000; 2000US-258675P.
(DYNA-) DYNAVAX TECHNOLOGIES CORP.
Fearon KL, Dina D;
WPI; 2002-657426/70.
Immunomodulatory polynucleotide for modulating an immune response in a
subject suffering from disorders associated with Th2-type immune
response, e.g. allergy, or infectious disease, comprises an
immunostimulatory sequence -
Claim 4; Page 20; 95pp; English.

The present invention describes an immunomodulatory polynucleotide (I)
comprising an immunostimulatory sequence (ISS). Also described: (1) an
immunomodulatory composition comprising (I); (2) an immunomodulatory
polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
biodegradable MC, where the MC is less than 10 micrometre in size; and
(3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
antibacterial and protozoacide activities, and can be used as a modulator
of immune response. (I) is useful for modulating an immune response in an
individual suffering from disorders associated with a Th2-type immune
response, especially an allergy or asthma, or an infectious disease. (I)

CC is also useful for increasing interferon-gamma (IFN-gamma) in an
 CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
 CC individual having a viral infection. (1) is further useful for
 CC ameliorating a symptom of an infectious disease caused by a cellular
 CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
 CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
 CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
 CC allergy-related disorder, in particular asthma in an individual. The
 CC present sequence represents an immunomodulatory oligonucleotide from
 CC the present invention.

CC Sequence 19 BP; 4 A; 4 C; 6 G; 5 T; 0 other;

Query Match 90.5%; Score 19; DB 24; Length 19;

Best Local Similarity 100.0%; Pred. No. 0.092; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCGTGAACGTTTCGAGATG 19

1 TCGTGAACGTTTCGAGATG 19

ABQ75181 standard; DNA; 22 BP.

05-NOV-2002 (first entry)

ISS immunomodulatory oligonucleotide SEQ ID NO:10.

Immunostimulatory sequence; ISS: immunomodulatory; immune response;
 allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
 idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
 malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
 immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
 virucide; antibacterial; protozoacide; ss.

Synthetic.

WO200252002-A2.

04-JUL-2002.

27-DEC-2001; 2001WO-US50821.

27-DEC-2000; 2000US-258675P.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Pearon KL, Dina D;

WPI; 2002-657426/70.

Immunomodulatory polynucleotide for modulating an immune response in a
 subject suffering from disorders associated with Th2-type immune
 response, e.g. allergy, or infectious disease, comprises an
 immunostimulatory sequence -

Example 1; Page 21; 95pp; English.

The present invention describes an immunomodulatory polynucleotide (1)
 comprising an immunostimulatory sequence (ISS). Also described: (1) an
 immunomodulatory composition comprising (1); (2) an immunomodulatory
 polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
 biodegradable MC, where the MC is less than 10 micrometre in size; and
 (3) a kit comprising (1). (1) has antiallergic, antiasthmatic, virucide,
 antibacterial and protozoacide activities, and can be used as a modulator
 of immune response. (1) is useful for modulating an immune response in an
 individual suffering from disorders associated with a Th2-type immune
 response, especially an allergy or asthma, or an infectious disease. (1)
 is also useful for increasing interferon-gamma (IFN-gamma) in an

CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
 CC individual having a viral infection. (1) is further useful for
 CC ameliorating a symptom of an infectious disease caused by a cellular
 CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
 CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
 CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
 CC allergy-related disorder, in particular asthma in an individual. The
 CC present sequence represents an immunomodulatory oligonucleotide from
 CC the present invention.

CC Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 other;

Query Match 90.5%; Score 19; DB 24; Length 22;

Best Local Similarity 100.0%; Pred. No. 0.091; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 TCGTGAACGTTTCGAGATG 19

4 TCGTGAACGTTTCGAGATG 22

ABQ75165 standard; DNA; 18 BP.

05-NOV-2002 (first entry)

ISS immunomodulatory oligonucleotide SEQ ID NO:14.

Immunostimulatory sequence; ISS: immunomodulatory; immune response;
 allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
 idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
 malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
 immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
 virucide; antibacterial; protozoacide; ss.

Synthetic.

WO200252002-A2.

04-JUL-2002.

27-DEC-2001; 2001WO-US50821.

27-DEC-2000; 2000US-258675P.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Pearon KL, Dina D;

WPI; 2002-657426/70.

Immunomodulatory polynucleotide for modulating an immune response in a
 subject suffering from disorders associated with Th2-type immune
 response, e.g. allergy, or infectious disease, comprises an
 immunostimulatory sequence -

Example 1; Page 20; 95pp; English.

The present invention describes an immunomodulatory polynucleotide (1)
 comprising an immunostimulatory sequence (ISS). Also described: (1) an
 immunomodulatory composition comprising (1); (2) an immunomodulatory
 polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
 biodegradable MC, where the MC is less than 10 micrometre in size; and
 (3) a kit comprising (1). (1) has antiallergic, antiasthmatic, virucide,
 antibacterial and protozoacide activities, and can be used as a modulator
 of immune response. (1) is useful for modulating an immune response in an
 individual suffering from disorders associated with a Th2-type immune
 response, especially an allergy or asthma, or an infectious disease. (1)
 is also useful for increasing interferon-gamma (IFN-gamma) in an
 individual having idiopathic pulmonary fibrosis, or IFN-alpha in an

CC individual having a viral infection. (1) is further useful for
 CC ameliorating a symptom of an infectious disease caused by a cellular
 CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
 CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
 CC symptom of an immunoglobulin E (IgE)-related disorder, preferably, an
 CC allergy-related disorder, in particular asthma in an individual. The
 CC present sequence represents an immunomodulatory oligonucleotide from
 CC the present invention.

CC Sequence 18 BP; 4 A; 4 C; 5 G; 5 T; 0 other;

CC Query Match 76.2%; Score 16; DB 24; Length 18;

CC Best Local Similarity 100.0%; Pred. No. 5;
 CC Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 4 TCGAAGCTTCGAGATG 19
 CC Db 3 TCGAAGCTTCGAGATG 18

CC RESULT 5

CC AAD24905 standard; DNA; 20 BP.

CC AAD24905;

CC 12-MAR-2002 (first entry)

CC Double-stranded immunostimulatory oligodeoxynucleotide (ISS-ODN).

CC Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;
 CC immune response; apoptosis; Alzheimer's disease; Parkinson's disease;
 CC rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;
 CC liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;
 CC amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;
 CC head injury damage; aplastic anaemia; tumour; organ transplantation;
 CC cerebral infarction; follicular lymphomas; systemic lupus erythematosus;
 CC viral infection; glomerulonephritis; apoptosis; autoimmune disorder;
 CC sepsis; immunostimulatory oligodeoxynucleotide; ISS-ODN; ds.

CC Unidentified.

CC WO200185910-A2.

CC 15-NOV-2001.

CC 04-MAY-2001; 2001WO-US14508.

CC 05-MAY-2000; 2000US-202274P.

CC 17-JAN-2001; 2001US-262321P.

CC (REGC) UNIV CALIFORNIA.

CC Raz E, Lois AF, Takabayashi K;

CC WPI; 2002-062244/08.

CC Modulating cell death or reducing DNA damage in eukaryotic cells,
 CC useful for reducing cell death in individual or organ, comprises
 CC contacting cell with agent modulating biological activity of
 CC DNA-dependent protein kinase -

CC Example 1; Page 31; 57pp; English.

CC The invention relates to a method for modulating cell death or reducing
 CC DNA damage in an eukaryotic cell by contacting the cell with an agent
 CC that modulates the biological activity of DNA-dependent protein kinase
 CC (DNA-PK). The invention also relates nucleic acids which modulate the
 CC immune response binding to Ku antigen, resulting in activation of DNA-PK.
 CC The method is useful for modulating cell death or reducing DNA damage in
 CC an eukaryotic cell, for treating any disorder resulting from a genotoxic
 CC insert to a cell e.g., necrosis, apoptosis. The method is also useful
 CC for treating cell death-related indications such as Alzheimer's disease,

CC Parkinson's disease, rheumatoid arthritis, septic shock, stroke,
 CC central nervous system inflammation, osteoporosis, degenerative liver
 CC disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,
 CC amyotrophic lateral sclerosis, myocardial infarction, head injury damage,
 CC acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral
 CC infarction, bypass heart surgery, organ transplantation. The method is
 CC also useful for treating follicular lymphomas, carcinomas, autolymphoma,
 CC disorders (systemic lupus erythematosus), hormone dependent tumours,
 CC immune mediated glomerulonephritis; apoptosis and viral infections. The
 CC present sequence is immunostimulatory oligodeoxynucleotide (ISS-ODN)
 CC used for identifying ISS-binding protein, which is used in the
 CC exemplification of the invention.

CC Sequence 20 BP; 6 A; 3 C; 6 G; 5 T; 0 other;

CC Query Match 71.4%; Score 15; DB 24; Length 20;

CC Best Local Similarity 100.0%; Pred. No. 19;
 CC Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 6 GAACGTTTCGAGATGA 20
 CC Db 6 GAACGTTTCGAGATGA 20

CC RESULT 6

CC AAV32079 standard; DNA; 22 BP.

CC AAV32079;

CC 09-SEP-1998 (first entry)

CC Nucleotide sequence of DY1018.

CC DY1018, beta-gal. ISS-PN/IMM; antigen; immune response; antibody;
 CC immunisation; anaplyxaxis; IgE; retinopathies; ss.
 CC synthetic.

CC Key Location/Qualifiers

CC modified_base 1.22

CC /tag= a
 CC /note= "phosphothioate backbone"

CC WO9816247-A1.

CC 23-APR-1998.

CC 09-OCT-1997; 97WO-US19004.

CC 11-OCT-1996; 96US-0028118.

CC (REGC) UNIV CALIFORNIA.

CC Carson DA, Raz E, Roman M;

CC WPI; 1998-261028/23.

CC New immunomodulatory compositions - comprising an antigen conjugated
 CC to a polynucleotide that contains an immunostimulatory sequence

CC Example 1; Page 36; 69pp; English.

CC This is the nucleotide sequence of DY1018, which is conjugated to
 CC beta-gal to form ISS-PN/IMM, comprising an immunomodulatory molecule
 CC (IMM), which comprises an antigen conjugated to a polynucleotide
 CC (PN) that contains at least one immunostimulatory nucleotide sequence
 CC (ISS). The conjugate synergistically boost the magnitude of the host
 CC immune response against an antigen to a level greater than the host
 CC immune response to either the IMM, antigen or ISS-PN alone. These
 CC responses to ISS-PN/IMM conjugates are particularly acute during
 CC the important early phase of the host immune response to an antigen.
 CC The ISS-PN/IMM conjugates boost both humoral (antibody) and cellular

(Th1 type) immune responses of the host. Thus, use of the method to boost the immune responsiveness of a host to subsequent challenge by a sensitising antigen without immunisation avoids the risk of Th2-mediated, immunisation-induced anaphylaxis by suppressing IgE production in response to the antigen challenge. The conjugates can also be used to combat pathogenic infection and to stimulate therapeutic angiogenesis to treat conditions in which localised blood flow plays a significant etiological role, e.g. retinopathies.

Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 19; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 GAACGTCGAGATGA 20
 |||||
 8 GAACGTCGAGATGA 22

RESULT 7
 AAX36624
 ID AAX36624 standard; DNA; 22 BP.
 AC AAX36624;
 XX
 XX 09-JUL-1999 (first entry)
 DT
 XX
 XX ISS-ODN DY1018 nucleotide sequence.
 DE
 XX
 KW Antigen-stimulated inflammation; immunostimulatory oligonucleotide;
 KW granulocyte-mediated tissue inflammation; Th2 type immune response;
 KW immune responsiveness modulation; idiopathic hypersensitivity; syndrome;
 KW cutaneous basophil hypersensitivity; ISS-ODN; asthma; nasal polyposis;
 KW allergic rhinitis; atopic dermatitis; allergic conjunctivitis;
 KW eosinophilic fasciitis; therapy; ss.
 KW
 XX
 OS Synthetic.
 XX
 XX WO9911275-A2.
 XX
 PD 11-MAR-1999.
 PD
 XX
 PE 04-SEP-1998; 98WO-US18382.
 XX
 PR 05-SEP-1997; 97US-0927120.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 XX Ray E;
 PI
 DR WPI, 1999-312404/26.
 XX
 XX Reducing antigen-stimulated granulocyte-mediated inflammation
 PT
 XX Example 2; Page 30; 69pp; English.
 PS
 XX This is the ISS-ODN DY1018 nucleotide sequence.
 CC The invention relates to a method for preventing or reducing
 CC antigen-stimulated, granulocyte-mediated tissue inflammation in a mammal,
 CC by administering an immunostimulatory oligonucleotide (ISS-ODN), where:
 CC (a) reduction in, or the absence of, a Th2 type immune response is
 CC measured; or (b) there is a reduction or absence of other clinical signs
 CC of inflammation in the host after antigen challenge. The method is used
 CC to reduce or suppress granulocyte-mediated inflammation in a host tissue,
 CC and to modulate the host's immune responsiveness to an antigen,
 CC particularly where the subject suffers from asthma, nasal polyposis,
 CC allergic rhinitis, atopic dermatitis, allergic conjunctivitis,
 CC eosinophilic fasciitis, idiopathic hypersensitivity syndrome, or
 CC cutaneous basophil hypersensitivity. Unlike prior art treatment by
 CC antigen immunisation, the method is an antigen-independent method,
 CC and avoids host production of both interleukin-4 (IL-4), which carries
 CC risk of anaphylaxis, and IL-5 which actually encourages granulocyte

adhesion to endothelia.

Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

6 GAACGTCGAGATGA 20
 |||||
 8 GAACGTCGAGATGA 22

RESULT 8
 AAV80105/C
 ID AAV80105 standard; DNA; 22 BP.
 AC AAV80105;
 XX
 XX 12-MAR-1999 (first entry)
 DT
 XX
 XX Oligo used in experiments for stimulation of cytokine production.
 DE
 XX
 KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
 KW
 XX
 OS Synthetic.
 XX
 XX WO9855495-A2.
 XX
 PD 10-DEC-1998.
 PD
 XX
 PE 05-JUN-1998; 98WO-US11578.
 XX
 PR 06-JUN-1997; 97US-0048793.
 XX
 PA (DNA-) DYNAX TECHNOLOGIES CORP.
 XX
 XX Dina D, Roman M, Schwartz D;
 PI
 DR WPI, 1999-059898/05.
 XX
 XX Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases
 PT
 XX
 XX Example 1; Page 29; 63pp; English.
 PS
 XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTCG, AACGTCG,
 CC GACGTCG, and GACGTCG. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80104 to AAV80116 represent
 CC oligonucleotides that were tested for immunostimulatory activity. These
 CC were used in experiments for the stimulation of cytokine production and
 CC were found to lack immunostimulatory activity. The invention provides
 CC specific claimed examples (AAV80096-103) of immunomodulatory sequences.

Sequence 22 BP; 5 A; 7 C; 4 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
 |||||
 DB 15 GAACGTTGAGATGA 1

RESULT 9
 AAV80096
 ID AAV80096 standard; DNA; 22 BP.

AAV80096;

DT 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.

OS Synthetic.

PN WO9855495-A2.

PD 10-DEC-1998.

PF 05-JUN-1998; 98WO-US11578.

PR 06-JUN-1997; 97US-0048793.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Dina D, Roman M, Schwartz D;

DR WPI; 1999-059898/05.

PT Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

PS Claim 7; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCC,
 CC GACGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 71.4%; Score 15; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
 |||||
 DB 8 GAACGTTGAGATGA 22

RESULT 10
 AAV80097
 ID AAV80097 standard; DNA; 22 BP.
 XX

AC AAV80097;
 XX
 DT 12-MAR-1999 (first entry)
 XX
 DE Immunomodulatory oligo comprising an ISS sequence.

KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.

OS Synthetic.

PN WO9855495-A2.

PD 10-DEC-1998.

PF 05-JUN-1998; 98WO-US11578.

PR 06-JUN-1997; 97US-0048793.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Dina D, Roman M, Schwartz D;

DR WPI; 1999-059898/05.

PT Immunostimulatory oligonucleotides regulate the immune system - and
 PT contain an immune-stimulating octanucleotide sequence; for treating
 PT cancer, allergic and infectious diseases

PS Claim 5; Page 29; 63pp; English.

XX The invention relates to immunomodulatory oligonucleotides that comprise
 CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
 CC sequences are selected from the group consisting of AACGTTCC, AACGTTCC,
 CC GACGTTCC, and GACGTTCC. The immunomodulatory sequences are used to treat
 CC patients needing immune regulation, such as those suffering from cancer,
 CC an allergic disease and asthma. They are also used to prevent infectious
 CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
 CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
 CC Bordetella pertussis, malarial plasmodia, leishmania, Trypanosoma and
 CC Schistosoma. The immunomodulatory sequences are used to screen for human
 CC immunostimulatory activity by incubating macrophage cells and the
 CC oligonucleotide; and determining the relative amount of Th1-biased
 CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
 CC specific claimed examples of such immunomodulatory oligonucleotides.

SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 20; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
 |||||
 DB 8 GAACGTTGAGATGA 22

RESULT 11
 AAV80102
 ID AAV80102 standard; DNA; 22 BP.

AAV80102;

DT 12-MAR-1999 (first entry)

DE Immunomodulatory oligo comprising an ISS sequence.

KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
 KW ISS: cancer; allergy; asthma; hepatitis B infection; papillomavirus;
 KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
 KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.


```

XX OS Synthetic.
XX FH Key
XX FT modified_base 11 Location/Qualifiers
XX FT /*tag= a
XX FT /note= "5-bromocytosine"
XX PN MO9855495-A2.
XX PD 10-DEC-1998.
XX PF 05-JUN-1998; 98WO-US11578.
XX PR 06-JUN-1997; 97US-0048793.
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX PI Dina D, Roman M, Schwartz D;
XX DR WPI; 1999-059898/05.
XX PT Immunostimulatory oligonucleotides regulate the immune system - and
XX PT contain an immune-stimulating octanucleotide sequence; for treating
XX PT cancer, allergic and infectious diseases
XX PS Claim 23; Page 30; 63pp; English.
XX CC The invention relates to immunomodulatory oligonucleotides that comprise
XX CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX CC sequences are selected from the group consisting of AACGTTCC, AACGTTGC,
XX CC GAGCTTCC, and GAGCTTGC. The immunomodulatory sequences are used to treat
XX CC patients needing immune regulation, such as those suffering from cancer,
XX CC an allergic disease and asthma. They are also used to prevent infectious
XX CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
XX CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
XX CC Schistosoma. The immunomodulatory sequences are used to screen for human
XX CC immunostimulatory activity by incubating macrophage cells and the
XX CC oligonucleotide; and determining the relative amount of Th1-biased
XX CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
XX CC specific claimed examples of such immunomodulatory oligonucleotides.
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 20; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 GAACGTTGAGATGA 20
XX DB 8 GAACGTTGAGATGA 22
XX
XX RESULT 12
XX ID AAV80103 standard; DNA; 22 BP.
XX AC AAV80103;
XX XX
XX DT 12-MAR-1999 (first entry)
XX DE Immunomodulatory oligo comprising an ISS sequence.
XX XX
XX KW Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
XX KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;
XX KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
XX KW B. pertussis; malaria; plasmodia; leishmania; Trypanosoma; Schistosoma.
XX OS Synthetic.
XX PF Key
XX FT modified_base 11 Location/Qualifiers

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```

XX FT /*tag= a
XX FT /note= "5-bromocytosine"
XX PN MO9855495-A2.
XX PD 10-DEC-1998.
XX PF 05-JUN-1998; 98WO-US11578.
XX PR 06-JUN-1997; 97US-0048793.
XX PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX PI Dina D, Roman M, Schwartz D;
XX DR WPI; 1999-059898/05.
XX PT Immunostimulatory oligonucleotides regulate the immune system - and
XX PT contain an immune-stimulating octanucleotide sequence; for treating
XX PT cancer, allergic and infectious diseases
XX PS Claim 24; Page 30; 63pp; English.
XX CC The invention relates to immunomodulatory oligonucleotides that comprise
XX CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
XX CC sequences are selected from the group consisting of AACGTTCC, AACGTTGC,
XX CC GAGCTTCC, and GAGCTTGC. The immunomodulatory sequences are used to treat
XX CC patients needing immune regulation, such as those suffering from cancer,
XX CC an allergic disease and asthma. They are also used to prevent infectious
XX CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
XX CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
XX CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
XX CC Schistosoma. The immunomodulatory sequences are used to screen for human
XX CC immunostimulatory activity by incubating macrophage cells and the
XX CC oligonucleotide; and determining the relative amount of Th1-biased
XX CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
XX CC specific claimed examples of such immunomodulatory oligonucleotides.
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 20; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 GAACGTTGAGATGA 20
XX DB 8 GAACGTTGAGATGA 22
XX
XX RESULT 13
XX ID AAC64051 standard; DNA; 22 BP.
XX AC AAC64051;
XX XX
XX DT 15-FEB-2001 (first entry)
XX DE Immunostimulatory CpG phosphorothioate oligodeoxynucleotide.
XX XX
XX KW CpG oligodeoxynucleotide; phosphorothioate; immunostimulatory; ISS ODN;
XX KW enhanced antigen presentation; antigen-presenting cell; APC;
XX KW T-cell activation; tumour cell; tumour antigen; cancer immunotherapy;
XX KW vaccine; ss.
XX OS Synthetic.
XX PF 26-OCT-2000.
XX PF 11-APR-2000; 2000WO-US09664.
XX PR 15-APR-1999; 99US-0292278.

```

XX (REGC) UNIV CALIFORNIA.
 XX
 XX Raz E, Martin-Orozco E;
 XX
 XX WPI; 2000-679548/66.
 XX
 XX Enhancing antigen-presentation capabilities of T-cells for cancer
 PT immunotherapy, by contacting cells with an immunostimulatory
 PT oligonucleotide -
 XX
 XX Example I; Page 18; 42pp; English.
 XX
 CC The invention relates to a method of inducing activation of T-cells
 CC to respond to an antigen, comprising contacting antigen-presenting cells
 CC (APC) with an immunostimulatory oligodeoxynucleotide (ISS-ODN). The APCs
 CC thus treated have enhanced antigen presenting capabilities compared to
 CC antigen-activated APCs. APCs with enhanced antigen-presentation
 CC capabilities then present the antigen to T-cells. The method is useful
 CC for cancer immunotherapy. The ISS-ODN is used to enhance the tumour
 CC antigen presenting capacity of tumour cells, thereby inducing T-cell
 CC activation, and is therefore useful for treating tumours. Additionally,
 CC tumour cells treated with an ISS-ODN ex vivo are useful as vaccines.
 CC ISS-ODN treated APCs are induced to take up antigen through upregulation
 CC of Fe-receptor expression, to present antigen through upregulation of
 CC major histocompatibility complex (MHC) Class I and II expression and
 CC CD4 expression, to produce co-stimulatory factors (B7 and CD40), to
 CC provide cell-to-cell adhesion through upregulation of intercellular
 CC adhesion molecule (ICAM) expression, and to increase Th1 stimulatory
 CC cytokine production, all at levels greater than that achieved through
 CC contact of APC with antigen alone. The present sequence represents
 CC a phosphorothioate Cpg ISS-ODN used in the exemplifications of the
 CC invention.
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 QY Query Match 71.4%; Score 15; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 GAACGTTGAGATGA 20
 8 GAACGTTGAGATGA 22
 RESULT 14
 AAA96253
 ID AAA96253 standard; DNA; 22 BP.
 AC AAA96253;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 DE Sequence of a stabilised oligonucleotide with antitumour activity.
 XX
 KW Antitumour; immunostimulatory oligonucleotide; tumour; anaplasia;
 KW glioblastoma; medulloblastoma; neuroblastoma; carcinoma; ss.
 XX
 OS Synthetic.
 XX
 PN WO200056342-A2.
 XX
 PD 28-SEP-2000.
 XX
 PF 17-MAR-2000; 2000WO-FR00676.
 XX
 FR 19-MAR-1999; 99FR-0003433.
 PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
 PA (INRM) INST NAT SANTE & RECH MEDICALE.
 XX
 PI Carpentier A;
 XX

DR WPI; 2000-602192/57.
 XX
 XX Use of stabilized oligonucleotides as antitumor agents, particularly
 PT against nervous system tumors, have optimal activity and are not toxic
 PT -
 XX
 XX Example 2; Page 16; 57pp; French.
 XX
 CC The present sequence represents a stabilised oligonucleotide which has
 CC antitumour activity. The oligonucleotide comprises an octamer motif
 CC of the type 5'-purine-purine-CG-pyrimidine-pyrimidine-X-X-3', where
 CC the pair X-X is AT, AA, CT or TT. The oligonucleotides are
 CC immunostimulatory, and are not toxic. They may be adapted for use in
 CC animals or humans. The stabilised oligonucleotides are used for
 CC treating tumours, of any type and any degree of anaplasia, particularly
 CC human tumours in the peripheral or central nervous systems, specifically
 CC glioblastomas, medulloblastomas, neuroblastomas, melanomas or carcinomas.
 XX
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 QY Query Match 71.4%; Score 15; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 6 GAACGTTGAGATGA 20
 8 GAACGTTGAGATGA 22
 RESULT 15
 AAA90458
 ID AAA90458 standard; DNA; 22 BP.
 AC AAA90458;
 XX
 DT 10-JAN-2001 (first entry)
 XX
 DE Cpg adjuvant oligonucleotide, SEQ ID NO:19.
 XX
 KW Cpg oligonucleotide; Cpg motif; adjuvant; microdroplet emulsion;
 KW microemulsion; adsorbent microparticle; vaccine; Th1 immune response;
 KW viral infection; bacterial infection; parasitic infection; HCV; HBV;
 KW hepatitis C virus; hepatitis B virus; herpes simplex virus; HSV; HIV;
 KW human immunodeficiency virus; cytomegalovirus; CMV; influenza virus;
 KW rabies virus; cholera; diphtheria; tetanus; pertussis;
 KW Helicobacter pylori; Haemophilus influenzae; malaria; ss.
 XX
 OS Synthetic.
 XX
 PN WO200050006-A2.
 XX
 PD 31-AUG-2000.
 XX
 PF 09-FEB-2000; 2000WO-US03331.
 XX
 PR 26-FEB-1999; 99US-0121858.
 PR 29-JUL-1999; 99US-0146391.
 PR 28-OCT-1999; 99US-0161997.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI O'Hagan D, Olt GS, Donnelly J, Kazaz J, Ugozzoli M, Singh M,
 PI Barackman J;
 XX
 DR WPI; 2000-587123/55.
 XX
 PT Microemulsion having an adsorbent surface comprising a microdroplet
 PT emulsion consisting of a metabolizable oil and an emulsifying agent
 PT which is a detergent, useful as a vaccine to treat bacterial, viral,
 PT and parasitic infection -
 XX
 PS Claim 17; Page 40; 95pp; English.
 XX

CC The invention relates to a microdroplet emulsion (microemulsion) with an
CC adsorbent surface, and which comprises a metabolisable oil and an
CC emulsifying agent (a detergent). It also relates to a composition
CC comprising the microemulsion and a microparticle with an adsorbent
CC surface, where the microparticle comprises a polymer selected from a
CC poly(alpha-hydroxy acid), a polyhydroxy butyric acid, a
CC polycaprolactone, a polyorthoester, a polyamide, and a
CC polycyanoacrylate, and a second detergent. The surface of the
CC microparticles efficiently adsorb biologically active macromolecules such
CC as DNA, polypeptides, antigens, hormones, pharmaceuticals, enzymes,
CC mediators of transcription or translation, metabolic intermediates and
CC adjuvants. Additionally, a second biologically active molecule may be
CC encapsulated within the microparticle. The microemulsion can be used in
CC methods of immunising a host animal, particularly a human, against a
CC viral, bacterial or parasitic infection, and in methods of increasing a
CC Th1 immune response. The microemulsions (having the appropriate antigens
CC adsorbed) may be particularly used as vaccines for hepatitis C virus
CC (HCV), hepatitis B virus (HBV), herpes simplex virus (HSV), human
CC immunodeficiency virus (HIV), cytomegalovirus (CMV), influenza virus, and
CC rabies virus; the bacteria which cause cholera, diphtheria, tetanus and
CC pertussis; Helicobacter pylori and Haemophilus influenzae; and
CC malaria-causing parasites. Sequences AAA30447-A30467 represent Th1
CC lymphocyte stimulating oligonucleotides containing at least one Cpg motif
CC which are claimed for use as adjuvants in the compositions of the
CC invention.

CC SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
|||
Db 8 GAACGTTGAGATGA 22

RESULT 16

AAA14467
ID AAA14467 standard; DNA; 22 BP.

AC AAA14467;

DT 21-AUG-2000 (first entry)

DB Immunostimulatory oligonucleotide (ISS-ODN) DY1018.

KW Immunostimulatory oligonucleotide; adjuvant; mucosal immunity;
KW secretory immunoglobulin A production; sIgA; Th1 phenotype; ds.

OS Synthetic.

PN WO200020039-A1.

PD 13-APR-2000.

PF 15-SEP-1999; 99WO-US21203.

PR 05-OCT-1998; 98US-0167039.

PA (REGC) UNIV CALIFORNIA.

PI Raz E, Horner AA, Carson DA;

DR WPI; 2000-303647/26.

PT Immunostimulatory oligonucleotide adjuvant induces mucosal immunity to
PT an antigen in a mammalian host through production of secretory
PT immunoglobulin A -

PS Claim 8; Page 21; 64pp; English.

CC The invention relates to a method of inducing mucosal immunity to an

CC antigen in a mammalian host, including the the production of secretory
CC immunoglobulin A (sIgA). Immune protection in the mucosa (the principal
CC site of entry of most foreign antigens) is mediated by mucosa-associated
CC lymphoid tissue, epithelial and distinct B-cell, T-cell and accessory
CC cell sub-populations. The primary immune response which characterises
CC the induction of mucosal immunity to an antigen is sIgA production by
CC activated B-cells. The method comprises introducing an immunostimulatory
CC oligonucleotide (ISS-ODN) and the antigen into host mucosa, where the
CC ISS-ODN includes a core nucleotide sequence. The core nucleotide
CC sequence is 5'-Purine-Purine-C-G-Pyrimidine-Pyrimidine-3', specific
CC examples of which are AACGTT, AGCGTC and GACGTT (SEQ ID Nos 1-3). A
CC specific example of an ISS-ODN is DY1018 (AAA14467). The ISS-ODN is used
CC as an adjuvant with an antigen for stimulating mucosal immunity. The
CC level of sIgA production induced in the host is at least 3 times the
CC magnitude of sIgA production achievable in response to introduction of
CC antigen alone into the mucosal tissue and is equivalent or greater than
CC the magnitude of sIgA production achievable in response to introduction
CC of the antigen and cholera toxin adjuvant into the mucosal tissue. The
CC host immune response is stimulated to antigen specific IgA production,
CC biased towards the Th1 phenotype while antigen-induced IgE production is
CC avoided. The adjuvant has little or no known toxicity in mammals and its
CC efficacy is comparable to that of cholera toxin which is used as a
CC mucosal adjuvant. The present sequence represents the immunostimulatory
CC oligonucleotide DY1018.

CC SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
|||
Db 8 GAACGTTGAGATGA 22

RESULT 17

AAA38065
ID AAA38065 standard; DNA; 22 BP.

AC AAA38065;

DT 24-AUG-2000 (first entry)

DB Immunostimulatory sequence (ISS) #1.

KW Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW gp120; human immunodeficiency virus; HIV; immune response; infection;
KW development; ss.

OS Synthetic.

PN WO200021556-A1.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23677.

PR 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Tighe H, Raz E, Schwartz D, Takabayashi K;

DR WPI; 2000-317846/27.

PT Anti-HIV composition comprises immunostimulatory polynucleotides and
PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
PT response against HIV in an HIV infected individual -

PS Claim 3; Page 16; 65pp; English.

CC

CC The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory composition which comprises a gp120
 CC conjugated to an immunomodulatory polynucleotide, or is proximately
 CC associated to it and not conjugated, is used for modulating or
 CC stimulating a specific immune response against gp120 in an individual by
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
 CC is also used for suppressing or delaying development of HIV infection in
 CC an individual infected with HIV or an individual at risk of infection
 CC with HIV, respectively. It is also used for treating an individual
 CC infected with HIV in need of immune modulation.

CC Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
 |||||
 DB 8 GAACGTCGAGATGA 22

RESULT 18

AAA38066
 ID AAA38066 standard; DNA; 22 BP.

AC AAA38066;

DT 24-AUG-2000 (first entry)

DE Immunostimulatory sequence (ISS) #2.

KM Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;
 development; ss.

OS Synthetic.

FN WO200021556-A1.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23677.

PR 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

PT Anti-HIV composition comprises immunostimulatory polynucleotides and
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
 PT response against HIV in an HIV infected individual -

PS Disclosure; Page 16; 65pp; English.

CC The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory composition which comprises a gp120
 CC conjugated to an immunomodulatory polynucleotide, or is proximately
 CC associated to it and not conjugated, is used for modulating or
 CC stimulating a specific immune response against gp120 in an individual by
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
 CC is also used for suppressing or delaying development of HIV infection in
 CC an individual infected with HIV or an individual at risk of infection

CC with HIV, respectively. It is also used for treating an individual
 CC infected with HIV in need of immune modulation.

CC Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
 |||||
 DB 8 GAACGTCGAGATGA 22

RESULT 19

AAA38071
 ID AAA38071 standard; DNA; 22 BP.

AC AAA38071;

DT 24-AUG-2000 (first entry)

DE Immunostimulatory sequence (ISS) #7.

KM Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;
 development; ss.

OS Synthetic.

FN WO200021556-A1.

PD 20-APR-2000.

PF 08-OCT-1999; 99WO-US23677.

PR 09-OCT-1998; 98US-0103733.

PR 07-OCT-1999; 99US-0415186.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Tighe H, Raz E, Schwartz D, Takabayashi K;

XX WPI; 2000-317846/27.

PT Anti-HIV composition comprises immunostimulatory polynucleotides and
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
 PT response against HIV in an HIV infected individual -

PS Disclosure; Page 17; 65pp; English.

CC The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory composition which comprises a gp120
 CC conjugated to an immunomodulatory polynucleotide, or is proximately
 CC associated to it and not conjugated, is used for modulating or
 CC stimulating a specific immune response against gp120 in an individual by
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
 CC is also used for suppressing or delaying development of HIV infection in
 CC an individual infected with HIV or an individual at risk of infection
 CC with HIV, respectively. It is also used for treating an individual
 CC infected with HIV in need of immune modulation.

CC Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 21; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 6 GAACGTCGAGATGA 20
 |||||
 8 GAACGTCGAGATGA 22
 Db

RESULT 20
 AAA8072
 ID AAA8072 standard; DNA; 22 BP.
 AC AAA8072;
 XX
 XX 24-APR-2000 (first entry)
 DT
 XX Immunostimulatory sequence (ISS) #7.
 DE
 XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
 KW gp120; human immunodeficiency virus; HIV; immune response; infection;
 KM development; ss.
 XX
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT modified_base 11
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "5-Bromocytosine"
 FT modified_base 15
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "5-Bromocytosine"
 FT
 FT
 XX WO200021556-A1.
 XX
 XX PD 20-APR-2000.
 XX
 XX PF 08-OCT-1999; 99WO-US2677.
 XX
 XX PR 09-OCT-1998; 98US-0103733.
 XX PR 07-OCT-1999; 99US-0415186.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 XX Tigue H, Raz E, Schwartz D, Takabayashi K;
 PI WPI; 2000-317846/27.
 XX
 XX Anti-HIV composition comprises immunostimulatory polynucleotides and
 PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
 PT response against HIV in an HIV infected individual
 XX
 PS Disclosure; Page 17; 65pp; English.
 XX
 XX The present invention relates to an immunostimulatory composition
 CC comprising a human immunodeficiency virus (HIV) antigen, and an
 CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
 CC (ISS). This sequence represents an ISS that can be used in the
 CC composition. An immunostimulatory composition which comprises a gp120
 CC conjugated to an immunomodulatory polynucleotide, or is proximately
 CC associated to it and not conjugated, is used for modulating or
 CC stimulating a specific immune response against gp120 in an individual by
 CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
 CC is also used for suppressing or delaying development of HIV infection in
 CC an individual infected with HIV or an individual at risk of infection
 CC with HIV, respectively. It is also used for treating an individual
 CC infected with HIV in need of immune modulation.
 CC
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 SQ
 Query Match 71.4%; Score 15; DB 21; Length 22;

Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 6 GAACGTCGAGATGA 20
 |||||
 8 GAACGTCGAGATGA 22
 Db

RESULT 21
 AA255876
 ID AA255876 standard; DNA; 22 BP.
 AC AA255876;
 XX
 XX 10-APR-2000 (first entry)
 DT
 XX Immunomodulatory oligonucleotide SEQ ID NO: 1.
 DE
 XX Immunomodulation; immunostimulatory sequence; adjuvant;
 KW Th1 immune response; cytotoxic T-cell; cytokine; cancer; allergy;
 KM asthma; immunosuppression; ss.
 XX
 XX Mus musculus.
 OS
 XX Synthetic.
 OS
 XX
 FH Key Location/Qualifiers
 FT modified_base 1.22
 FT /*tag= a
 FT /note= "Phosphorothioate linkages"
 FT misc_feature 9..16
 FT /*tag= b
 FT /note= "Immunostimulatory sequence (ISS)"
 FT
 FT
 XX WO9962923-A2.
 XX
 XX PD 09-DEC-1999.
 XX
 XX PF 04-JUN-1999; 99WO-US12538.
 XX
 XX PR 05-JUN-1998; 98US-0088310.
 XX PR 01-JUN-1999; 99US-0324191.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 XX Schwartz D;
 PI WPI; 2000-105687/09.
 XX
 XX Novel immunomodulatory oligonucleotide used to induce a Th1-type immune
 PT response, e.g. to tumor antigens
 PT
 XX
 PS Example 1; Page 35; 54pp; English.
 XX
 XX Sequences AA255876-255877 and AA255880-255886 represent immunomodulatory
 CC oligonucleotides comprising an immunostimulatory sequence (ISS, e.g.,
 CC AACGTC, AACGTT, AGCGTC, AGCGCT, AGCGTT, GACGTC, GACGTT, GCCTTC,
 CC AACGTC and GACGTC). The invention relates to oligonucleotides
 CC comprising one or more ISSs, where the ISS comprises at least
 CC one modified cytosine with an electron-withdrawing moiety at
 CC position C-5 or C-6 of the base. Sequences AA255877 and AA255880-255886
 CC contain ISSs comprising at least one bromocytosine, whereas sequence
 CC AA255876 contains an unmodified ISS. The immunomodulatory
 CC oligonucleotides have an adjuvant-like effect; when formulated with an
 CC antigen, the oligonucleotides stimulate production of Th1-type cytokines,
 CC and induce a Th1-type immune response (activation of cytotoxic T cells),
 CC while simultaneously downregulating the Th2-type response. The Th1
 CC response is particularly effective for control of viruses and
 CC intracellular parasites. The immunomodulatory oligonucleotides are used,
 CC particularly when formulated with an antigen or a facilitator, for
 CC modulating immune responses. Such compositions may be used in tumour
 CC therapy, in treatment of allergy (including asthma), for inducing a
 CC vigorous cellular response (against a virus, bacterium, fungus or
 CC protozoan), and also in contraceptive vaccines based on sperm antigens.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ

Query Match 71.4%; Score 15; DB 21; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
|||
8 GAACGTTGAGATGA 22

RESULT 22

AAH43338
ID AAH43338 standard; DNA; 22 BP.

AC AAH43338;

DT 13-DEC-2001 (first entry)

DE Immunomodulatory polynucleotide 1018.

XX Immunomodulation; inflammation; gastrointestinal tract;

KW ulcerative colitis; Crohn's disease; inflammatory bowel disease;
KM diarrhoea; rectal bleeding; weight loss; colon; weight; lesion; ss.

OS Synthetic.

PN WO200162207-A2.

PD 30-AUG-2001.

PF 22-FEB-2001; 2001WO-US06034.

PR 23-FEB-2000; 2000US-0184256.

PA (REGC) UNIV CALIFORNIA.

PI Raz E, Rachmilewitz D;

DR WPI; 2001-565393/63.

PT Ameliorating gastrointestinal inflammation e.g. inflammatory bowel
XX disease involves administering an immunomodulatory nucleic acid -

PS Claim 7; Page 28; 58pp; English.

XX The sequences given in AAH43338-48 represent immunomodulatory
CC polynucleotides which may be used to ameliorate inflammation of
CC the gastrointestinal tract by administering a nucleic acid comprising
CC one of these sequences. These polynucleotides all comprise an
CC immunomodulatory polynucleotide sequence of 5'-CpG-3' (I). The
CC nucleotides may be used for ameliorating or reducing gastrointestinal
CC inflammation e.g. chronic or acute gastrointestinal inflammation,
CC ulcerative colitis, Crohn's disease caused by inflammatory bowel
CC disease; diarrhoea, rectal bleeding, weight loss; to reduce colon
CC weight and colon lesions; to reduce a colonic inflammation. The
CC immunomodulatory polynucleotides treat inflammatory bowel disease
CC satisfactorily and effectively and have little or no toxicity even
CC at a high dosage of 50000 micro-g. They also reduce the risk of
CC colonic cancer by treating ulcerative colitis.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ

Query Match 71.4%; Score 15; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
|||
8 GAACGTTGAGATGA 22

RESULT 23
AA514664
ID AA514664 standard; DNA; 22 BP.

AC AA514664;

DT 18-DEC-2001 (first entry)

DE Immunostimulatory sequence, ISS #1.

XX Immunostimulatory sequence; ISS; ds; antiviral; immunogen;

KW respiratory syncytial virus; RSV; influenza virus; rhinovirus;
KM adenovirus; measles virus; mumps virus; parainfluenza virus;
KM rubella virus; poxvirus; parvovirus; hantavirus; varicella virus.

OS Respiratory syncytial virus.

OS Synthetic.

PH Key Location/Qualifiers

FT modified_base 1..22

FT /tag= a
FT /label= OTHER
/note= "Phosphorothioate Backbone"

PN WO200168116-A2.

PD 20-SEP-2001.

PF 12-MAR-2001; 2001WO-US07839.

PR 10-MAR-2000; 2000US-186683P.

PR 09-MAR-2001; 2001US-0802686.

PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.

PI Van Nest G;

DR WPI; 2001-607438/69.

PT Suppressing a respiratory syncytial virus infection by administering an
XX immunostimulatory sequence at the site of infection is useful to
XX prevent and treat lower respiratory tract viral infections -

PS Claim 5; Page 37; 40pp; English.

XX The invention relates to suppressing a respiratory syncytial virus (RSV)
CC infection in an exposed individual, comprising administering a
CC polynucleotide comprising an immunostimulatory sequence (ISS) comprising
CC the sequence 5'-C, G-3', where an RSV antigen is not administered.
CC The invention is used to prevent and treat respiratory syncytial
CC virus infection of the lower respiratory tract and other viruses
CC including influenza virus, rhinovirus, adenovirus, measles virus, mumps
CC virus, parainfluenza virus, rubella virus, poxvirus, parvovirus,
CC hantavirus and varicella virus. A kit for carrying out
CC the administration is also included. Unlike the prior art antiviral agent
CC ribavirin, which is a potential teratogen, the invention provides a
CC treatment which does not carry unacceptable side effects. Other prior art
CC medicaments treat the symptoms only, whilst the invention treats the
CC infection. The present sequence is an ISS of the invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ

Query Match 71.4%; Score 15; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
|||
8 GAACGTTGAGATGA 22

RESULT 24

AA514665

ID AAS14665 standard; DNA; 22 BP.
 XX AAS14665;
 AC
 XX 18-DEC-2001 (first entry)
 DT
 XX Immunostimulatory sequence, ISS #2.
 DE
 XX Immunostimulatory sequence; ISS; ds; antiviral; immunogen;
 KM respiratory syncytial virus; RSV; influenza virus; rhinovirus;
 KM adenovirus; measles virus; mumps virus; parainfluenza virus;
 KM rubella virus; poxvirus; parvovirus; hantavirus; varicella virus.
 XX
 OS Respiratory syncytial virus.
 OS Synthetic.
 PN WO200168116-A2.
 PD 20-SEP-2001.
 XX
 PF 12-MAR-2001; 2001WO-US07839.
 XX
 PR 10-MAR-2000; 2000US-188583P.
 PR 09-MAR-2001; 2001US-0802686.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Van Nest G;
 XX
 DR WPI; 2001-607438/69.
 XX
 PT Suppressing a respiratory syncytial virus infection by administering an
 PT immunostimulatory sequence at the site of infection is useful to
 PT prevent and treat lower respiratory tract viral infections -
 XX
 PS Disclosure; Page 15; 40pp; English.
 XX
 SS The invention relates to suppressing a respiratory syncytial virus (RSV)
 CC infection in an exposed individual, comprising administering a
 CC polynucleotide comprising an immunostimulatory sequence (ISS) comprising
 CC the sequence 5'-C, G-3', where an RSV antigen is not administered.
 CC The invention is used to prevent and treat respiratory syncytial
 CC virus infection of the lower respiratory tract and other viruses
 CC including influenza virus, rhinovirus, adenovirus, measles virus, mumps
 CC virus, parainfluenza virus, rubella virus, poxvirus, parvovirus,
 CC hantavirus and varicella virus. A kit for carrying out
 CC the administration is also included. Unlike the prior art antiviral agent
 CC ribavirin, which is a potential teratogen, the invention provides a
 CC treatment which does not carry unacceptable side effects. Other prior art
 CC medications treat the symptoms only, whilst the invention treats the
 CC infection. The present sequence is an ISS of the invention.
 CC
 XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;
 SQ

Query Match 71.4%; Score 15; DB 22; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
 |||||
 DB 8 GAACGTTGAGATGA 22

RESULT 25
 AAH75992
 ID AAH75992 standard; DNA; 22 BP.
 XX
 AC AAH75992;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 XX Immunomodulatory oligonucleotide #1.
 DE
 XX

KM Immunomodulatory; immunostimulatory; Th1-type immune response;
 KM Th2-type immune response; interferon; idiopathic pulmonary fibrosis;
 KM viral infection; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..22
 FT /+tag= a
 FT /mod_base= "OTHER"
 FT /note= "Phosphorothioate oligonucleotide"
 XX
 PN WO200168143-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 12-MAR-2001; 2001WO-US07843.
 XX
 PR 10-MAR-2000; 2000US-0188557.
 PR 09-MAR-2001; 2001US-0802376.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 XX
 PI Van Nest G, Tuck S;
 XX
 DR WPI; 2001-582389/65.
 XX
 PT Immunomodulatory polynucleotide/microcarrier complexes comprise an
 PT immunostimulatory sequence containing polynucleotide linked to a
 PT nonbiodegradable microcarrier -
 XX
 PS Claim 11; Page 49; 61pp; English.
 XX
 SS The present invention relates to immunomodulatory polynucleotide/
 CC microcarrier complexes. The complexes comprise an immunostimulatory
 CC sequence (ISS), e.g. the present sequence, linked to a nonbiodegradable
 CC microcarrier provided that if the microcarrier is gold, latex or magnetic
 CC then the linkage is not biotin/avidin. The complex is useful for
 CC modulating an immune response (especially stimulating a Th1-type response
 CC or suppressing a Th2-type response), increasing interferon-gamma
 CC (especially in a patient suffering from idiopathic pulmonary fibrosis),
 CC increasing interferon-alpha (especially in patients suffering from viral
 CC infection) and reducing levels of IgE.
 CC
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 SQ

Query Match 71.4%; Score 15; DB 22; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
 |||||
 DB 8 GAACGTTGAGATGA 22

RESULT 26
 AAH75993
 ID AAH75993 standard; DNA; 22 BP.
 XX
 AC AAH75993;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 XX Immunomodulatory oligonucleotide #2.
 DE
 XX Immunomodulatory; immunostimulatory; Th1-type immune response;
 KM Th2-type immune response; interferon; idiopathic pulmonary fibrosis;
 KM viral infection; ss.
 XX
 OS Synthetic.
 XX
 PN WO200168143-A2.
 XX

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PD 20-SEP-2001.
XX
XX 12-MAR-2001; 2001WO-US07843.
XX
XX 10-MAR-2000; 2000US-0188557.
XX
XX 09-MAR-2001; 2001US-0802376.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Van Nest G, Tuck S;
XX
XX WPI, 2001-582389/65.
XX
XX Immunomodulatory polynucleotide/microcarrier complexes comprise an
XX immunostimulatory sequence containing polynucleotide linked to a
XX nonbiodegradable microcarrier -
XX
XX PS Disclosure; Page 18; 61pp; English.
XX
XX The present invention relates to immunomodulatory polynucleotide/
XX microcarrier complexes. The complexes comprise an immunostimulatory
XX sequence (ISS), e.g. the present sequence, linked to a nonbiodegradable
XX microcarrier provided that if the microcarrier is gold, latex or magnetic
XX then the linkage is not biotin/avidin. The complex is useful for
XX modulating an immune response (especially stimulating a Th1-type response
XX or suppressing a Th2-type response), increasing interferon-gamma
XX (especially in a patient suffering from idiopathic pulmonary fibrosis),
XX increasing interferon-alpha (especially in patients suffering from viral
XX infection) and reducing levels of IgE.
XX
XX SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match          71.4%; Score 15; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 GAACGTTGAGATGA 20
        |||||
        8 GAACGTTGAGATGA 22

Db      8 GAACGTTGAGATGA 22

RESULT 27
AAH42533
ID AAH42533 standard; DNA; 22 BP.
XX
XX AAH42533;
XX
XX 01-OCT-2001 (first entry)
XX
XX Phosphorothioate beta-gal/immunostimulatory oligonucleotide.
XX
XX Anaphylactic hypersensitivity; immunomodulatory nucleic acid; vaccine;
XX anaphylaxis-associated symptom; IgE; histamine; phosphorothioate; ss.
XX
XX OS Synthetic.
XX
XX WO200145750-A1.
XX
XX 28-JUN-2001.
XX
XX 20-DEC-2000; 2000WO-US35064.
XX
XX 21-DEC-1999; 99US-0171830.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Raz E, Horner AA;
XX
XX WPI, 2001-475812/51.
XX
XX Reducing risk of anaphylactic hypersensitivity response to an allergen
XX in a subject, by administering an immunomodulating nucleic acid
XX molecule comprising a specific sequence -

```

```

XX
XX Example 1; Page 22; 39pp; English.
XX
XX The specification describes a method for reducing a symptom associated
XX with anaphylactic hypersensitivity or risk of anaphylactic response in
XX a subject. The method comprises administering to an individual a
XX nucleic acid molecule comprising an immunomodulatory nucleic acid
XX molecule (INA) comprising the sequence 5'-C-G-3' to reduce
XX anaphylaxis-associated symptom. The method is useful for reducing a
XX symptom associated with anaphylactic hypersensitivity, including an
XX elevated IgE level, elevated histamine level, constriction of the
XX airways and difficult breathing which can lead to anaphylactic reaction
XX or anaphylactic shock, thereby reducing the risk of death. The present
XX sequence represents a beta-gal/immunostimulatory sequence, which was
XX used as a vaccine to protect against the development of anaphylactic
XX hypersensitivity.
XX
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match          71.4%; Score 15; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      6 GAACGTTGAGATGA 20
        |||||
        8 GAACGTTGAGATGA 22

Db      8 GAACGTTGAGATGA 22

RESULT 28
AAH73439
ID AAH73439 standard; DNA; 22 BP.
XX
XX AAH73439;
XX
XX 01-OCT-2001 (first entry)
XX
XX Immunomodulatory nucleic acid.
XX
XX G3PDH gene; immunomodulatory oligonucleotide; infection; mycobacterium;
XX intracellular pathogen; anti-pathogenic; ss.
XX
XX OS Unidentified.
XX
XX WO200155341-A2.
XX
XX 02-AUG-2001.
XX
XX 30-JAN-2001; 2001WO-US03029.
XX
XX 31-JAN-2000; 2000US-0179353.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Raz E, Kornbluth R, Catanzaro A, Hayashi T, Carson DA;
XX
XX WPI, 2001-483234/52.
XX
XX Treating infection of intracellular pathogen e.g., Mycobacterium, in a
XX subject, involves administering immunomodulatory nucleic acid molecule
XX to inhibit intracellular replication of intracellular pathogen -
XX
XX Examples; Page 26; 54pp; English.
XX
XX The present invention describes a method of treating an infection caused
XX by an intracellular pathogen, involving administering to the patient an
XX immunomodulatory nucleic acid and an anti-pathogenic agent. This is
XX particularly useful in the treatment of mycobacterial infections. The
XX present sequence is an immunomodulatory nucleic acid described in the
XX exemplification of the invention.
XX
XX SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match          71.4%; Score 15; DB 22; Length 22;

```


Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
|||||
DB 8 GAACGTCGAGATGA 22

RESULT 29
AAH44109
ID AAH44109 standard; DNA; 22 BP.
XX
AC AAH44109;
XX
DT 12-SEP-2001 (first entry)
XX
DE 5' terminal NH2 group and a 3' terminal rhodamine moiety oligonucleotide.
XX
KM Peptide nucleic acid; intracellular protein delivery; cationic lipid;
KM PNA; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT modified_base 1 /tag= a
FT /mod_base= OTHER
FT /note= "T has been modified at the 5' terminal with
FT an NH2 group"
FT modified_base 22 /tag= b
FT /mod_base= OTHER
FT /note= "A has been modified at the 3' terminal with
FT rhodamine"
XX
PN WO200143778-A1.
XX
PD 21-JUN-2001.
XX
PF 15-DEC-2000; 2000WO-US33969.
XX
PR 17-DEC-1999; 99US-0172441.
XX
PA (GENE-) GENE THERAPY SYSTEMS INC.
PI Feigner PI, Zelphect O;
XX
XX WPI; 2001-398080/42.
DR
XX
PT Composition useful for intracellular delivery of a protein, comprises a
PT protein in operative association with a cationic intracellular delivery
PT vehicle comprising a cationic lipid, which is adapted to fuse with a
PT cell membrane
XX
PS Example 3; Page 18; 33pp; English.
XX
CC The present invention describes a composition (I) for intracellular
CC delivery of a protein, comprising a protein in operative association
CC with a cationic intracellular delivery vehicle comprising a cationic
CC lipid, where the intracellular delivery vehicle is adapted to fuse with
CC a cell membrane, therefore effecting intracellular delivery of the
CC associated protein. Also described is a method for delivering a protein
CC to a cell involving providing the protein associated with a cationic
CC lipid in such a manner so as to form an intracellular delivery
CC composition, and contacting the delivery composition with a cell
CC membrane of a cell, such that the cationic lipid forms an association
CC with a cell membrane and delivers the protein into the cell. (I) is
CC useful in the preparation of a medicament for intracellular delivery of
CC a therapeutic or prophylactic protein. (I) is useful for delivering
CC antibodies to intracellular proteins to neutralise their activity, and
CC to introduce therapeutically useful, proteins, peptides or small
CC molecules. (I) is useful for the in vitro or in vivo delivery of
CC antibodies or peptides which block the function of specific intracellular

CC proteins and affect cellular metabolism, cell viability or virus
CC replication. (I) is useful for delivering any protein of interest,
CC including therapeutically useful proteins (e.g. tumour suppressor
CC proteins, cystic fibrosis transmembrane regulator (CFTR), adenosine
CC deaminase (ADA), hexoseaminidase A, peptides, wild type protein
CC counterparts of mutant proteins and cell surface receptors) such as
CC those for cytokines (e.g., interleukins, interferons, colony stimulating
CC factors) and peptide hormones. The present sequence represents a peptide
CC nucleic acid (PNA) oligonucleotide which is used in an example from the
CC present invention for intracellular delivery of proteins.
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTCGAGATGA 20
|||||
DB 8 GAACGTCGAGATGA 22

RESULT 30
AAH41573
ID AAH41573 standard; DNA; 22 BP.
XX
AC AAH41573;
XX
DT 24-AUG-2001 (first entry)
XX
DE Immunostimulatory sequence (ISS) SEQ ID NO.1.
XX
KM Immunostimulatory sequence; ISS; immunomodulatory; immune response;
KM antigen; anti-allergic; modulation; Th1 lymphocyte stimulation; allergy;
KM Th1-associated cytokine; Th2 lymphocyte suppression; cytokine; ss.
XX
OS Synthetic.
XX
PN WO200135991-A2.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-US31385.
XX
PR 15-NOV-1999; 99US-0165467.
PR 14-NOV-2000; 2000US-0713136.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
PI Tuck S, Van Nest G;
XX
XX WPI; 2001-329209/34.
DR
XX
PT Populations of conjugate molecules comprising polynucleotide
PT immunostimulatory sequences polynucleotides and antigens, useful for
PT controlling immune responses -
XX
PS Example 1; Page 30; 97pp; English.
XX
CC The present invention describes immunomodulatory populations (I) and
CC (II) of conjugate molecules (CME) comprising immunostimulatory sequences
CC (ISS) of polynucleotides and antigens. The extent of conjugation affects
CC the immunological properties (e.g. the extent of antigen-specific
CC antibody formation, including Th1-associated antibody formation) so the
CC conjugates are used for altering the type and extent of immune response.
CC (I) and (II) have immunomodulatory, immunosuppressive and anti-allergic
CC activities, and can be used in the modulation of immune responses via
CC the stimulation of Th1 lymphocytes and Th1-associated cytokines, and
CC suppression of Th2 lymphocytes and cytokines. The populations (I) and
CC (II) of conjugate molecules may be used for modulating immune responses
CC in individuals e.g. for the treatment of an allergic condition. (I) and
CC (II) may be used to modulate immune responses and therefore prevent
CC potentially harmful reactions to antigens. The present sequence

CC represents an ISS polynucleotide which is used in the exemplification
 CC of the present invention.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
 |||||
 DB 8 GAACGTCGAGATGA 22

RESULT 31
 AAH41574
 ID AAH41574 standard; DNA; 22 BP.

XX AAH41574;

XX 24-AUG-2001 (first entry)

XX Immunostimulatory sequence (ISS) SEQ ID NO:2.

XX Immunostimulatory sequence; ISS; immunomodulatory; immune response;
 KW antigen; anti-allergic; modulation; Th1 lymphocyte stimulation; allergy;
 KW Th1-associated cytokine; Th2 lymphocyte suppression; cytokine; ss.

XX Synthetic.

XX WO200135991-A2.

XX 25-MAY-2001.

XX 15-NOV-2000; 2000WO-US31385.

XX 15-NOV-1999; 99US-0165467.

XX 14-NOV-2000; 2000US-0713136.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Tuck S, Van Nest G;

XX WPI; 2001-329209/34.

XX Populations of conjugate molecules comprising polynucleotide
 PT immunostimulatory sequences polynucleotides and antigens, useful for
 PT controlling immune responses -

XX Disclosure; Page 30; 97pp; English.

XX The present invention describes immunomodulatory populations ((I) and
 CC ((II)) of conjugate molecules (CMs) comprising immunostimulatory sequences
 CC ((ISS)) of polynucleotides and antigens. The extent of conjugation affects
 CC the immunological properties (e.g. the extent of antigen-specific
 CC antibody formation, including Th1-associated antibody formation) so the
 CC conjugates are used for altering the type and extent of immune response.
 CC ((I) and ((II)) have immunomodulatory, immunosuppressive and anti-allergic
 CC activities, and can be used in the modulation of immune responses via
 CC the stimulation of Th1 lymphocytes and Th1-associated cytokines, and
 CC suppression of Th2 lymphocytes and cytokines. The populations ((I) and
 CC ((II)) of conjugate molecules may be used for modulating immune responses
 CC in individuals e.g. for the treatment of an allergic condition. ((I) and
 CC ((II)) may be used to modulate immune responses and therefore prevent
 CC potentially harmful reactions to antigens. The present sequence
 CC represents an ISS polynucleotide which is used in the exemplification
 CC of the present invention.

XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
 |||||
 DB 8 GAACGTCGAGATGA 22

RESULT 32
 AAH20403
 ID AAH20403 standard; DNA; 22 BP.

XX AAH20403;

XX 03-AUG-2001 (first entry)

XX Cpg motif containing oligonucleotide SEQ ID #21.

XX Immune system stimulator; Cpg motif; Cpg receptor; Cpg-R; antibacterial;
 KW immune response; vaccine adjuvant; tumour immunotherapy; allergy;
 KW anti-inflammatory; cystic fibrosis; sepsis; heart disease; chlamydia;
 KW inflammatory bowel disease; arthritis; multiple sclerosis; ss.

XX Unidentified.

XX Key Location/Qualifiers

FT modified_base 1..22
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Phosphorothioate internucleoside linkages"

XX WO200132877-A2.

XX 10-MAY-2001.

XX 01-NOV-2000; 2000WO-USA1735.

XX 02-NOV-1999; 99US-0163157.

XX 24-NOV-1999; 99US-0167389.

XX (CHIR) CHIRON CORP.

XX Mackichan ML;

XX WPI; 2001-343486/36.

XX Novel Cpg receptor and nucleic acid molecule encoding the receptor, for
 PT modulating immune response and for identifying compounds of therapeutic
 PT use which bind and/or modulate the activity of the receptor -

XX Example 1; Page 14; 41pp; English.

XX Unmethylated CG dinucleotide sequences are commonly found in bacterial
 CC DNA, and have been found to stimulate the innate immune system. Natural
 CC killer and T cells are activated by exposure to oligonucleotides
 CC containing Cpg motifs. Oligonucleotides containing Cpg motifs can be used
 CC as adjuvants in vaccines. The present invention relates to a Cpg
 CC receptor. The Cpg receptor contains a Toll homology domain (THD). The
 CC Toll receptor family are associated with responses to pathogens. Cpg
 CC oligonucleotides may act as stimulators of various immune responses. The
 CC Cpg receptor or cells expressing the receptor are useful for identifying
 CC a compound which binds to or modulates an activity of the Cpg receptor.
 CC The compounds are useful in e.g. vaccine adjuvants promoting
 CC cell-mediated immune responses, antibacterials, (e.g. protection from
 CC listeria infection), tumour immunotherapy, allergy treatment, (e.g.
 CC suppressing IgE in human PMC, shifting from Th2 to Th1) and as
 CC anti-inflammatory agents (e.g. for use in cystic fibrosis, sepsis, heart
 CC disease, chlamydia, inflammatory bowel disease, arthritis and multiple
 CC sclerosis). The present sequence represents a Cpg motif containing
 CC oligonucleotide used in examples demonstrating that Cpg oligonucleotides
 CC can activate the MAPK pathways and NF-kappaB.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;

Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
|||
DB 8 GAACGTCGAGATGA 22

RESULT 33

AAAF77040 ID AAF77040 standard; DNA; 22 BP.

AAAF77040; AC

15-MAY-2001 (first entry)

Immunomodulatory DNA.

Module; immune; antigen; immunostimulatory; ds.

Synthetic.

WO200112223-A2.

22-FEB-2001.

18-AUG-2000; 2000WO-US22835.

19-AUG-1999; 99US-0149768.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Van Nest G;

WPI; 2001-211136/21.

Modulating immune response to a second antigen in humans involves

administering an immunostimulatory polynucleotide comprising an

immunostimulatory sequence and a first antigen

Claim 31; Page 15; 63pp; English.

The present invention relates to modulating an immune response to

a second antigen in an individual, involving immunostimulatory polynucleotide

administering to the individual an immunomodulatory polynucleotide

comprising an immunostimulatory sequence (ISS) and a first antigen.

Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
|||
DB 8 GAACGTCGAGATGA 22

RESULT 34

AAAF77041 ID AAF77041 standard; DNA; 22 BP.

AAAF77041; AC

15-MAY-2001 (first entry)

Immunostimulatory DNA #1.

Module; immune; antigen; immunostimulatory; ds.

Synthetic.

WO200112223-A2.

XX 22-FEB-2001.

18-AUG-2000; 2000WO-US22835.

19-AUG-1999; 99US-0149768.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Van Nest G;

WPI; 2001-211136/21.

Modulating immune response to a second antigen in humans involves

administering an immunostimulatory polynucleotide comprising an

immunostimulatory sequence and a first antigen

Disclosure; Page 15; 63pp; English.

The present invention relates to modulating an immune response to

a second antigen in an individual, involving immunostimulatory polynucleotide

administering to the individual an immunomodulatory polynucleotide

comprising an immunostimulatory sequence (ISS) and a first antigen.

Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 22;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
|||
DB 8 GAACGTCGAGATGA 22

RESULT 35

AAAF29800 ID AAF29800 standard; DNA; 22 BP.

AAAF29800; AC

12-APR-2001 (first entry)

Cholera toxin immunostimulatory nucleotide sequence.

Immunostimulatory nucleotide sequence; immune response; cancer;

antibody production; IFNgamma release; CTL activity; Th1 response;

infection; allergy; ds.

Unidentified.

WO200102007-A1.

11-JAN-2001.

30-JUN-2000; 2000WO-US18229.

02-JUL-1999; 99US-0347343.

(REGC) UNIV CALIFORNIA.

Raz E, Kobayashi H;

WPI; 2001-138066/14.

Enhancing immune response against pathogen or antigen associated with

infectious diseases, an allergen or cancer, involves administering

immunostimulatory nucleotide sequence prior to antigen exposure -

Example 1; Page 14; 47pp; English.

The present invention describes a method for enhancing an immune response

to a substance, comprising administering an immunostimulatory nucleotide

CC sequence to a subject prior to exposure to the substance. This can be
 CC used to enhance antibody production, IFNgamma release, CTL activity and
 CC Th1 related effects. The method can be used in the prevention and
 CC treatment of allergies, cancer and infections.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 71.4%; Score 15; DB 22; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 19;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 6 GAACGTCGAGATGA 20

XX 8 GAACGTCGAGATGA 22

XX RESULT 36

XX AAC82107

XX AAC82107 standard; DNA; 22 BP.

XX AAC82107;

XX 07-MAR-2001 (first entry)

XX Oligonucleotide ODNCT DNA SEQ ID NO 2.

XX Immunogenic; human immunodeficiency virus; immunostimulatory sequence;

XX ISS; beta-chemokine; anti-HIV; AIDS; Th1 immune response; primer;

XX HIV-specific cytotoxic T lymphocyte response; phosphorothioate; ss.

XX Synthetic.

XX WO200067787-A2.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12495.

XX 06-MAY-1999; 99US-0132762.

XX 25-AUG-1999; 99US-0150667.

XX (IMMU-) IMMUNE RESPONSE CORP.

XX Moss RB;

XX WPI; 2001-031804/04.

XX Human immunodeficiency virus (HIV) compositions useful for immunizing

XX and inhibiting AIDS in mammals, comprises HIV devoid of outer envelope

XX protein and an immunostimulatory nucleic acid sequence -

XX Example 1; Page 26; 64p; English.

XX This invention describes a novel immunogenic composition (I), comprising

XX a whole-killed human immunodeficiency virus (HIV) devoid of outer

XX envelope, protein gp120, an isolated nucleic acid molecule containing an

XX immunostimulatory sequence (ISS) and an adjuvant, which enhances

XX beta-chemokine levels in a mammal. The products of the invention have

XX anti-HIV activity. (I) is useful for immunizing and for inhibiting AIDS

XX in a mammal. The mammal can be a primate such as a human. (HIV

XX seronegative or seropositive humans) or a rodent, in particular the

XX primate is a pregnant mother or an infant. (I) can induce potent Th1

XX immune responses against a broad spectrum of HIV epitopes and provides a

XX strong HIV-specific cytotoxic T lymphocyte response.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 71.4%; Score 15; DB 22; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 19;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 6 GAACGTCGAGATGA 20

XX 8 GAACGTCGAGATGA 22

XX RESULT 36

XX AAC82107

XX AAC82107 standard; DNA; 22 BP.

XX AAC82107;

XX 07-MAR-2001 (first entry)

XX Oligonucleotide ODNCT DNA SEQ ID NO 2.

XX Immunogenic; human immunodeficiency virus; immunostimulatory sequence;

XX ISS; beta-chemokine; anti-HIV; AIDS; Th1 immune response; primer;

XX HIV-specific cytotoxic T lymphocyte response; phosphorothioate; ss.

XX Synthetic.

XX WO200067787-A2.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12495.

XX 06-MAY-1999; 99US-0132762.

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XX WPI; 2001-031804/04.

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XX Example 1; Page 26; 64p; English.

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XX immunostimulatory sequence (ISS) and an adjuvant, which enhances

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XX in a mammal. The mammal can be a primate such as a human. (HIV

XX seronegative or seropositive humans) or a rodent, in particular the

XX primate is a pregnant mother or an infant. (I) can induce potent Th1

XX immune responses against a broad spectrum of HIV epitopes and provides a

XX strong HIV-specific cytotoxic T lymphocyte response.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 71.4%; Score 15; DB 22; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 19;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 6 GAACGTCGAGATGA 20

XX 8 GAACGTCGAGATGA 22

XX RESULT 36

XX AAC82107

XX AAC82107 standard; DNA; 22 BP.

XX AAC82107;

XX 07-MAR-2001 (first entry)

XX Oligonucleotide ODNCT DNA SEQ ID NO 2.

XX Immunogenic; human immunodeficiency virus; immunostimulatory sequence;

XX ISS; beta-chemokine; anti-HIV; AIDS; Th1 immune response; primer;

XX HIV-specific cytotoxic T lymphocyte response; phosphorothioate; ss.

XX Synthetic.

XX WO200067787-A2.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12495.

XX 06-MAY-1999; 99US-0132762.

XX 25-AUG-1999; 99US-0150667.

XX (IMMU-) IMMUNE RESPONSE CORP.

XX Moss RB;

XX WPI; 2001-031804/04.

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XX immunostimulatory sequence (ISS) and an adjuvant, which enhances

XX beta-chemokine levels in a mammal. The products of the invention have

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XX in a mammal. The mammal can be a primate such as a human. (HIV

XX seronegative or seropositive humans) or a rodent, in particular the

XX primate is a pregnant mother or an infant. (I) can induce potent Th1

XX immune responses against a broad spectrum of HIV epitopes and provides a

XX strong HIV-specific cytotoxic T lymphocyte response.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 71.4%; Score 15; DB 22; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 19;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 6 GAACGTCGAGATGA 20

XX 8 GAACGTCGAGATGA 22

XX RESULT 36

XX AAC82107

XX AAC82107 standard; DNA; 22 BP.

XX AAC82107;

XX 07-MAR-2001 (first entry)

XX Oligonucleotide ODNCT DNA SEQ ID NO 2.

XX Immunogenic; human immunodeficiency virus; immunostimulatory sequence;

XX ISS; beta-chemokine; anti-HIV; AIDS; Th1 immune response; primer;

XX HIV-specific cytotoxic T lymphocyte response; phosphorothioate; ss.

XX Synthetic.

XX WO200067787-A2.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12495.

XX 06-MAY-1999; 99US-0132762.

XX 25-AUG-1999; 99US-0150667.

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XX Moss RB;

XX WPI; 2001-031804/04.

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XX protein and an immunostimulatory nucleic acid sequence -

XX Example 1; Page 26; 64p; English.

XX This invention describes a novel immunogenic composition (I), comprising

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XX envelope, protein gp120, an isolated nucleic acid molecule containing an

XX immunostimulatory sequence (ISS) and an adjuvant, which enhances

XX beta-chemokine levels in a mammal. The products of the invention have

XX anti-HIV activity. (I) is useful for immunizing and for inhibiting AIDS

XX in a mammal. The mammal can be a primate such as a human. (HIV

XX seronegative or seropositive humans) or a rodent, in particular the

XX primate is a pregnant mother or an infant. (I) can induce potent Th1

XX immune responses against a broad spectrum of HIV epitopes and provides a

XX strong HIV-specific cytotoxic T lymphocyte response.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 71.4%; Score 15; DB 22; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 19;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 6 GAACGTCGAGATGA 20

XX 8 GAACGTCGAGATGA 22

XX RESULT 36

XX AAC82107

XX AAC82107 standard; DNA; 22 BP.

XX AAC82107;

XX 07-MAR-2001 (first entry)

XX Oligonucleotide ODNCT DNA SEQ ID NO 2.

XX Immunogenic; human immunodeficiency virus; immunostimulatory sequence;

XX ISS; beta-chemokine; anti-HIV; AIDS; Th1 immune response; primer;

XX HIV-specific cytotoxic T lymphocyte response; phosphorothioate; ss.

XX Synthetic.

XX WO200067787-A2.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12495.

XX 06-MAY-1999; 99US-0132762.

XX 25-AUG-1999; 99US-0150667.

XX (IMMU-) IMMUNE RESPONSE CORP.

XX Moss RB;

XX WPI; 2001-031804/04.

XX Human immunodeficiency virus (HIV) compositions useful for immunizing

XX and inhibiting AIDS in mammals, comprises HIV devoid of outer envelope

XX protein and an immunostimulatory nucleic acid sequence -

XX Example 1; Page 26; 64p; English.

XX This invention describes a novel immunogenic composition (I), comprising

XX a whole-killed human immunodeficiency virus (HIV) devoid of outer

XX envelope, protein gp120, an isolated nucleic acid molecule containing an

XX immunostimulatory sequence (ISS) and an adjuvant, which enhances

XX beta-chemokine levels in a mammal. The products of the invention have

XX anti-HIV activity. (I) is useful for immunizing and for inhibiting AIDS

XX in a mammal. The mammal can be a primate such as a human. (HIV

XX seronegative or seropositive humans) or a rodent, in particular the

XX primate is a pregnant mother or an infant. (I) can induce potent Th1

XX immune responses against a broad spectrum of HIV epitopes and provides a

XX strong HIV-specific cytotoxic T lymphocyte response.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 71.4%; Score 15; DB 22; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 19;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 6 GAACGTCGAGATGA 20

XX 8 GAACGTCGAGATGA 22

XX RESULT 36

XX AAC82107

XX AAC82107 standard; DNA; 22 BP.

XX AAC82107;

XX 07-MAR-2001 (first entry)

XX Oligonucleotide ODNCT DNA SEQ ID NO 2.

XX Immunogenic; human immunodeficiency virus; immunostimulatory sequence;

XX ISS; beta-chemokine; anti-HIV; AIDS; Th1 immune response; primer;

XX HIV-specific cytotoxic T lymphocyte response; phosphorothioate; ss.

XX Synthetic.

XX WO200067787-A2.

XX 16-NOV-2000.

XX 05-MAY-2000; 2000WO-US12495.

XX 06-MAY-1999; 99US-0132762.

XX 25-AUG-1999; 99US-0150667.

XX (IMMU-) IMMUNE RESPONSE CORP.

XX Moss RB;

XX WPI; 2001-031804/04.

XX Human immunodeficiency virus (HIV) compositions useful for immunizing

XX and inhibiting AIDS in mammals, comprises HIV devoid of outer envelope

XX protein and an immunostimulatory nucleic acid sequence -

XX Example 1; Page 26; 64p; English.

XX This invention describes a novel immunogenic composition (I), comprising

XX a whole-killed human immunodeficiency virus (HIV) devoid of outer

XX envelope, protein gp120, an isolated nucleic acid molecule containing an

XX immunostimulatory sequence (ISS) and an adjuvant, which enhances

XX beta-chemokine levels in a mammal. The products of the invention have

XX anti-HIV activity. (I) is useful for immunizing and for inhibiting AIDS

XX in a mammal. The mammal can be a primate such as a human. (HIV

XX seronegative or seropositive humans) or a rodent, in particular the

XX primate is a pregnant mother or an infant. (I) can induce potent Th1

XX immune responses against a broad spectrum of HIV epitopes and provides a

XX strong HIV-specific cytotoxic T lymphocyte response.

XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

XX Query Match 71.4%; Score 15; DB 22; Length 22;

XX Best Local Similarity 100.0%; Pred. No. 19;

XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 6 GAACGTCGAGATGA 20

XX 8 GAACGTCGAGATGA 22

XX RESULT 36

XX AAC82107

XX AAC82107 standard; DNA; 22 BP.

XX AAC82107;

XX 07-MAR-2001 (first entry)

XX Oligonucleotide ODNCT DNA SEQ ID NO 2.

XX Immunogenic; human immunodeficiency virus; immunostimulatory sequence;

AC ABV73190;
 XX
 DT 08-JAN-2003 (first entry)
 XX
 XX Nucleotide sequence of an immunostimulatory oligonucleotide ISS-1.
 XX
 KW Immunomodulator; immunostimulant; antiinflammatory; antiasthmatic; Th2;
 KW antiallergic; dermatological; vaccine; gene therapy; immune response; ss.
 XX
 OS Synthetic.
 XX
 PN WO200274922-A2.
 XX
 PD 26-SEP-2002.
 XX
 PF 15-MAR-2002; 2002WO-US08207.
 XX
 PR 16-MAR-2001; 2001US-276865P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Broide DH, Raz E;
 DR WPI; 2002-740857/80.
 XX
 PT Suppressing a symptom of an allergic response in a subject, useful for
 PT preventing inflammation associated with allergy, comprises
 PT administering to an antigen-sensitized host first and second doses of
 PT an immunomodulatory nucleic acid -
 XX
 PS Examples; Page 27; 98pp; English.
 XX
 CC The invention relates to suppressing symptoms of allergic response that
 CC involves administering to an antigen-sensitized mammalian host a dose of
 CC a composition comprising an immunomodulatory nucleic acid, and a second
 CC dose of a composition comprising an immunomodulatory nucleic acid, about
 CC 1 day - 8 weeks after the first dose. The immunomodulatory nucleic acid
 CC comprises a nucleotide sequence comprising 5'-CG-3'. The methods are
 CC useful for suppressing a symptom of an allergic reaction in a subject,
 CC maintaining suppression of a Th2 immune response and maintaining
 CC stimulation of a Th1 immune response. One method is useful in preventing
 CC the onset of, or rapidly suppress, antigen-stimulated inflammation in a
 CC host. The immunostimulatory nucleic acids are useful in the treatment and
 CC prevention of inflammation associated with allergy, including antigen-
 CC stimulated granulocyte infiltration of tissue, such as occurs in the
 CC respiratory passages of asthmatics during an asthma attack, for boosting
 CC the immune responsiveness of a mammalian host to a sensitizing antigen,
 CC and for treating a host suffering from inflammatory conditions such as
 CC asthma, nasal polypsis, allergic rhinitis, atopic dermatitis, allergic
 CC conjunctivitis, eosinophil fasciitis, idiopathic hypereosinophilic
 CC syndrome, and cutaneous basophil hypersensitivity. The present sequence
 CC represents the nucleotide sequence of an immunomodulatory
 CC oligonucleotide.
 CC
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
 |||||
 DB 8 GAACGTTGAGATGA 22

RESULT 39
 ABO78627
 ID ABO78627 standard; DNA; 22 BP.
 XX
 AC ABO78627;
 XX
 DT 25-NOV-2002 (first entry)
 XX

DE ISS enhancing HIV-specific Th1 cytokine and humoral responses.
 XX
 KW Immunostimulatory sequence; ISS; Th1 cytokine response; humoral response;
 KW HIV; beta-chemokine; immunisation; AIDS; ss.
 XX
 OS Unidentified.
 XX
 PN WO200258726-A1.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US02077.
 XX
 PR 26-JAN-2001; 2001US-264476P.
 XX
 PA (IMMU-) IMMUNE RESPONSE CORP.
 XX
 PI Moss RB, Carlo DJ;
 DR WPI; 2002-643331/69.
 XX
 PT Treating an HIV-infected individual comprises treatment with
 PT anti-retroviral compound and immunization with an HIV immunogenic
 PT composition with structured cycles of anti-retroviral treatment and
 PT withdrawal from treatment -
 XX
 PS Disclosure; Page 15; 31pp; English.
 XX
 CC The present sequence represents an exemplary immunostimulatory sequence
 CC (ISS) which enhances HIV-specific Th1 cytokine and humoral responses,
 CC and also enhances both non-specific and HIV-specific beta-chemokine
 CC production. ISSs can be included in HIV immunogenic compositions of
 CC the invention. The specification describes a method for treating an
 CC HIV-infected individual, which comprises combining immunisation with an
 CC anti-retroviral compound, an HIV immunogenic composition with structured
 CC cycles of anti-retroviral treatment and withdrawal from treatment. The
 CC advantages of the method of the invention include a delay in the rebound
 CC to an unacceptably high viral load; a more rapid or sustained increase in
 CC HIV-specific CD4 T cell counts; a reduction or delay in the development
 CC of AIDS symptoms, including AIDS-related opportunistic infections; and
 CC a higher degree of patient compliance with treatment and fewer toxic side
 CC effects associated with long-term anti-retroviral drug treatment. The
 CC method is useful for treating an HIV-infected individual.
 CC
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGAGATGA 20
 |||||
 DB 8 GAACGTTGAGATGA 22

RESULT 40
 AAL44504
 ID AAL44504 standard; DNA; 22 BP.
 XX
 AC AAL44504;
 XX
 DT 08-NOV-2002 (first entry)
 XX
 DE Cpg motif oligonucleotide #12.
 XX
 KW Vaccine; immune response; microparticle; ds; adsorbent surface;
 KW poly(alpha-hydroxy acid); poly(hydroxy butyric acid); polycaprolactone;
 KW polyorthoester; polycyanoacrylate; detergent; submicron emulsion;
 KW viral infection; bacterial infection; parasitic infection;
 KW Cpg oligonucleotide.
 XX
 OS Unidentified.
 XX

```

PN WO200226209-A2.
XX
XX 04-APR-2002.
XX
XX 28-SEP-2001; 2001WO-US30540.
XX
XX 28-SEP-2000; 2000US-236105P.
XX
XX 30-AUG-2001; 2001US-315905P.
XX
XX (CHIR ) CHIRON CORP.
XX
XX O'hagan D, Otten G, Donnelly JJ, Polo JM, Barnett S, Singh M;
XX Ulmer J, Dubensky TW;
XX WPI; 2002-519084/55.
XX
XX A microparticle to which a biologically active macromolecule is
XX adsorbed, for use as a vaccine composition to treat viral, bacterial or
XX parasitic infections, comprises a polymer microparticle, a detergent
XX and a submicron emulsion -
XX
XX Disclosure; Page 46; 100pp; English.
XX
XX The invention relates to a method of raising an immune response in a host
XX animal. The method of the invention comprises administering a
XX microparticle that has an adsorbent surface to which a first biologically
XX active macromolecule (e.g. a nucleic acid) has been adsorbed. The
XX microparticle comprises a polymer microparticle of poly(alpha-hydroxy
XX acid), a polyhydroxy butyric acid, a polycaprolactone, a polyorthoester,
XX a polyanhydride, a detergent, and submicron emulsion. The method/
XX a microparticle of the invention is useful for immunizing a host animal
XX against viral, bacterial or parasitic infections. The present DNA
XX sequence represents a Cpg oligonucleotide of the invention.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 GAACGTTGCAGATGA 20
XX |||||
XX 8 GAACGTTGCAGATGA 22
XX
XX Db
XX
XX RESULT 41
XX ABQ75153
XX ID ABQ75153 standard; DNA; 22 BP.
XX
XX AC ABQ75153;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE ISS immunomodulatory oligonucleotide SEQ ID NO:2.
XX
XX KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
XX allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
XX idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
XX malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
XX immunoglobulin E; IGE-related disorder; antiallergic; antiasthmatic;
XX virucide; antibacterial; protozoacide; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_RNA 13
XX FT /*tag= a
XX FT /*note= "uracil"
XX
XX PN WO200252002-A2.
XX
XX PD 04-JUL-2002.
XX
XX

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PF 27-DEC-2001; 2001WO-US50821.
XX
XX 27-DEC-2000; 2000US-258675P.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Fearon KL, Dina D;
XX WPI; 2002-657426/70.
XX
XX Immunomodulatory polynucleotide for modulating an immune response in a
XX subject suffering from disorders associated with Th2-type immune
XX response, e.g. allergy, or infectious disease, comprises an
XX immunostimulatory sequence -
XX
XX Claim 4; Page 20; 95pp; English.
XX
XX The present invention describes an immunomodulatory polynucleotide (I)
XX comprising an immunostimulatory sequence (ISS). Also described: (1) an
XX immunomodulatory composition comprising (1); (2) an immunomodulatory
XX polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
XX biodegradable MC, where the MC is less than 10 micrometre in size; and
XX (3) a kit comprising (1). (1) has antiallergic, antiasthmatic, virucide,
XX antibacterial and protozoacide activities, and can be used as a modulator
XX of immune response. (1) is useful for modulating an immune response in an
XX individual suffering from disorders associated with a Th2-type immune
XX response, especially an allergy or asthma, or an infectious disease. (1)
XX is also useful for increasing interferon-gamma (IFN-gamma) in an
XX individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
XX individual having a viral infection. (1) is further useful for
XX ameliorating a symptom of an infectious disease caused by a cellular
XX pathogen such as mycobacterial disease, malaria, leishmaniasis,
XX toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
XX symptom of an immunoglobulin E (IGE)-related disorder, preferably an
XX allergy-related disorder, in particular asthma in an individual. The
XX present sequence represents an immunomodulatory oligonucleotide which
XX is specifically claimed in the present invention.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 5 T; 1 U; 0 other;
XX
XX QY Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 93.3%; Pred. No. 19;
XX Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 6 GAACGTTGCAGATGA 20
XX |||||
XX 8 GAACGTTGCAGATGA 22
XX
XX Db
XX
XX RESULT 42
XX ABQ75163
XX ID ABQ75163 standard; DNA; 22 BP.
XX
XX AC ABQ75163;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE ISS immunomodulatory oligonucleotide SEQ ID NO:12.
XX
XX KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
XX allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
XX idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
XX malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
XX immunoglobulin E; IGE-related disorder; antiallergic; antiasthmatic;
XX virucide; antibacterial; protozoacide; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT misc_RNA 13
XX FT /*tag= a
XX FT /*note= "uracil"
XX
XX PN WO200252002-A2.
XX
XX PD 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-US50821.
XX
XX

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XX 27-DEC-2000; 2000US-258675P.
PR
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
PA
XX Fearon KL, Dina D;
PI
XX WPI; 2002-657426/70.
DR
XX Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence
XX
XX Example 1; Page 20; 95pp; English.
PS
XX The present invention describes an immunomodulatory polynucleotide (I)
XX comprising an immunostimulatory sequence (ISS). Also described: (1) an
XX immunomodulatory composition comprising (1); (2) an immunomodulatory
XX polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
XX biodegradable MC, where the MC is less than 10 micrometre in size; and
XX (3) a kit comprising (1). (1) has anti-allergic, antiasthmatic, virucide,
XX antibacterial and protozoacide activities, and can be used as a modulator
XX of immune response. (1) is useful for modulating an immune response in an
XX individual suffering from disorders associated with a Th2-type immune
XX response, especially an allergy or asthma, or an infectious disease. (1)
XX is also useful for increasing interferon-gamma (IFN-gamma) in an
XX individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
XX individual having a viral infection. (1) is further useful for
XX ameliorating a symptom of an infectious disease caused by a cellular
XX pathogen such as mycobacterial disease, malaria, leishmaniasis,
XX toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
XX symptom of an immunoglobulin E (IgE)-related disorder, preferably an
XX allergy-related disorder, in particular asthma in an individual. The
XX present sequence represents an immunomodulatory oligonucleotide from
XX the present invention.
SQ
XX Sequence 22 BP; 5 A; 4 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 6 GAAGCTTCGAGATGA 20
Db 8 GAAGCTTCGAGATGA 22

RESULT 43
AB075173
ID AB075173 standard; DNA; 22 BP.
XX
XX AB075173;
AC
XX
XX 05-NOV-2002 (first entry)
DT
XX
XX ISS immunomodulatory oligonucleotide SEQ ID NO:22.
DE
XX Immunostimulatory sequence; ISS: immunomodulatory; immune response;
XX allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
XX idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
XX malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
XX immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
XX virucide; antibacterial; protozoacide; ss.
XX
XX Synthetic.
XX
XX WO200252002-A2.
XX
XX 04-JUL-2002.
XX
XX 27-DEC-2001; 2001WO-US50821.
XX

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```

PR 27-DEC-2000; 2000US-258675P.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
PA
XX Fearon KL, Dina D;
PI
XX WPI; 2002-657426/70.
DR
XX Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence
XX
XX Example 1; Page 20; 95pp; English.
PS
XX The present invention describes an immunomodulatory polynucleotide (I)
XX comprising an immunostimulatory sequence (ISS). Also described: (1) an
XX immunomodulatory composition comprising (1); (2) an immunomodulatory
XX polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
XX biodegradable MC, where the MC is less than 10 micrometre in size; and
XX (3) a kit comprising (1). (1) has anti-allergic, antiasthmatic, virucide,
XX antibacterial and protozoacide activities, and can be used as a modulator
XX of immune response. (1) is useful for modulating an immune response in an
XX individual suffering from disorders associated with a Th2-type immune
XX response, especially an allergy or asthma, or an infectious disease. (1)
XX is also useful for increasing interferon-gamma (IFN-gamma) in an
XX individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
XX individual having a viral infection. (1) is further useful for
XX ameliorating a symptom of an infectious disease caused by a cellular
XX pathogen such as mycobacterial disease, malaria, leishmaniasis,
XX toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
XX symptom of an immunoglobulin E (IgE)-related disorder, preferably an
XX allergy-related disorder, in particular asthma in an individual. The
XX present sequence represents an immunomodulatory oligonucleotide from
XX the present invention.
SQ
XX Sequence 22 BP; 4 A; 6 C; 6 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 TCGTCGAACGTTCCA 15
Db 1 TCGTCGAACGTTCCA 15

RESULT 44
AB075206
ID AB075206 standard; DNA; 22 BP.
XX
XX AB075206;
AC
XX
XX 05-NOV-2002 (first entry)
DT
XX
XX ISS immunomodulatory oligonucleotide SEQ ID NO:40.
DE
XX Immunostimulatory sequence; ISS: immunomodulatory; immune response;
XX allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
XX idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
XX malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
XX immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
XX virucide; antibacterial; protozoacide; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX misc_RNA 14
XX /*tag= a
XX /note= "uracil"
XX
XX WO200252002-A2.
XX

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PD 04-JUL-2002.
 XX 27-DEC-2001; 2001WO-US50821.
 PF 27-DEC-2001; 2001WO-US50821.
 XX 27-DEC-2000; 2000US-258675P.
 PR 27-DEC-2000; 2000US-258675P.
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 PI Fearon KL, Dina D;
 XX WPI; 2002-657426/70.
 DR WPI; 2002-657426/70.
 XX Immunomodulatory polynucleotide for modulating an immune response in a
 PT subject suffering from disorders associated with Th2-type immune
 PT response, e.g. allergy, or infectious disease, comprises an
 PT immunostimulatory sequence -
 PS Disclosure; Page 22; 95pp; English.
 XX The present invention describes an immunomodulatory polynucleotide (1)
 CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
 CC immunomodulatory composition comprising (1); (2) an immunomodulatory
 CC polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
 CC biodegradable MC, where the MC is less than 10 micrometre in size; and
 CC (3) a kit comprising (1). (1) has anti-allergic, antiasthmatic, virucide,
 CC antibacterial and protozoacide activities, and can be used as a modulator
 CC of immune response. (1) is useful for modulating an immune response in an
 CC individual suffering from disorders associated with a Th2-type immune
 CC response, especially an allergy or asthma, or an infectious disease. (1)
 CC is also useful for increasing interferon-gamma (IFN-gamma) in an
 CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
 CC individual having a viral infection. (1) is further useful for
 CC ameliorating a symptom of an infectious disease caused by a cellular
 CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
 CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
 CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
 CC allergy-related disorder, in particular asthma in an individual. The
 CC present sequence represents an immunomodulatory oligonucleotide from
 CC the present invention.
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 5 T; 1 U; 0 other;
 SQ
 Query Match 71.4%; Score 15; DB 24; Length 22;
 Best Local Similarity 93.3%; Pred. No. 19;
 Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GAACGTTGAGATGA 20
 Db 8 GAACGTTGAGATGA 22
 RESULT 45
 ABQ75211
 ID ABQ75211 standard; DNA; 22 BP.
 XX
 AC ABQ75211;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE ISS immunomodulatory oligonucleotide SEQ ID NO:45.
 XX
 KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
 KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
 KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
 KW malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
 KW immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
 KW virucide; antibacterial; protozoacide; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 2 /*tag= a
 FT

FT /mod_base= OTHER
 FT /note= "5-bromocytosine"
 FT modified_base 5
 FT /*tag= b
 FT /mod_base= OTHER
 FT /note= "5-bromocytosine"
 FT
 PN W0200252002-A2.
 XX
 PD 04-JUL-2002.
 XX
 XX 27-DEC-2001; 2001WO-US50821.
 PF 27-DEC-2001; 2001WO-US50821.
 XX 27-DEC-2000; 2000US-258675P.
 PR 27-DEC-2000; 2000US-258675P.
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 PI Fearon KL, Dina D;
 XX WPI; 2002-657426/70.
 DR WPI; 2002-657426/70.
 XX Immunomodulatory polynucleotide for modulating an immune response in a
 PT subject suffering from disorders associated with Th2-type immune
 PT response, e.g. allergy, or infectious disease, comprises an
 PT immunostimulatory sequence -
 PS Example 1; Page 22; 95pp; English.
 XX The present invention describes an immunomodulatory polynucleotide (1)
 CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
 CC immunomodulatory composition comprising (1); (2) an immunomodulatory
 CC polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
 CC biodegradable MC, where the MC is less than 10 micrometre in size; and
 CC (3) a kit comprising (1). (1) has anti-allergic, antiasthmatic, virucide,
 CC antibacterial and protozoacide activities, and can be used as a modulator
 CC of immune response. (1) is useful for modulating an immune response in an
 CC individual suffering from disorders associated with a Th2-type immune
 CC response, especially an allergy or asthma, or an infectious disease. (1)
 CC is also useful for increasing interferon-gamma (IFN-gamma) in an
 CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
 CC individual having a viral infection. (1) is further useful for
 CC ameliorating a symptom of an infectious disease caused by a cellular
 CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
 CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
 CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
 CC allergy-related disorder, in particular asthma in an individual. The
 CC present sequence represents an immunomodulatory oligonucleotide from
 CC the present invention.
 XX Sequence 22 BP; 5 A; 2 C; 7 G; 6 T; 2 other;
 SQ
 Query Match 71.4%; Score 15; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 GAACGTTGAGATGA 20
 Db 8 GAACGTTGAGATGA 22
 RESULT 46
 ABQ75212
 ID ABQ75212 standard; DNA; 22 BP.
 XX
 AC ABQ75212;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE ISS immunomodulatory oligonucleotide SEQ ID NO:46.
 XX
 KW Immunostimulatory sequence; ISS: immunomodulatory; immune response;
 KW allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
 KW idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;

KV	malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW	immunoglobulin E; IgE-related disorder; antiallergic; antiasthmatic;
KM	virucide; antibacterial; protozoacide; ss.
XX	
OS	Synthetic.
XX	
FH	Key
FT	modified_base
FT	Location/Qualifiers
FT	5
FT	/tag= a
FT	/mod_base= OTHER
FT	/note= "5-Bromocytosine"
XX	
PN	WO200252002-A2.
XX	
PD	04-JUL-2002.
XX	
PF	27-DEC-2001; 2001WO-US50821.
XX	
PR	27-DEC-2000; 2000US-258675P.
XX	
PA	(DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX	
PI	Fearon KL, Dina D;
XX	
DR	WPI; 2002-657426/70.
XX	
PT	Immunomodulatory polynucleotide for modulating an immune response in a
PT	subject suffering from disorders associated with Th2-type immune
PT	response, e.g. allergy, or infectious disease, comprises an
PT	immunostimulatory sequence -
PS	
PS	Example 1; Page 22; 95pp; English.
XX	
CC	The present invention describes an immunomodulatory polynucleotide (I)
CC	comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC	immunomodulatory composition comprising (I); (2) an immunomodulatory
CC	polynucleotide/microcarrier (IMP/MC) complex, comprising (I) linked to a
CC	biodegradable MC, where the MC is less than 10 micrometre in size; and
CC	(3) a kit comprising (I). (I) has antiallergic, antiasthmatic, virucide,
CC	antibacterial and protozoacide activities, and can be used as a modulator
CC	of immune response. (I) is useful for modulating an immune response in an
CC	individual suffering from disorders associated with a Th2-type immune
CC	response, especially an allergy or asthma, or an infectious disease. (I)
CC	is also useful for increasing interferon-gamma (IFN-gamma) in an
CC	individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC	individual having a viral infection. (I) is further useful for
CC	ameliorating a symptom of an infectious disease caused by a cellular
CC	pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC	toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC	symptom of an immunoglobulin B (IgB)-related disorder, preferably an
CC	allergy-related disorder, in particular asthma in an individual. The
CC	present sequence represents an immunomodulatory oligonucleotide from
CC	the present invention.
XX	
SQ	Sequence 22 BP; 5 A; 3 C; 7 G; 6 T; 1 other;
XX	
OY	Query Match 71.4%; Score 15; DB 24; Length 22;
DB	Best Local Similarity 100.0%; Pred. No. 19;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0
XX	
OY	6 GAACGTTGCAGATGA 20
DB	
DB	8 GAACGTCGAGATGA 22
XX	
RESULT 47	
ID	ABQ75259 standard; DNA; 22 BP.
XX	
AC	ABQ75259;
XX	
DT	05-NOV-2002 (first entry)
XX	

DE ISS immunomodulatory positive control oligonucleotide SEQ ID NO:59.

KX Immunostimulatory sequence; ISS: immunomodulatory; immune response;
KM allergy; asthma; infectious disease; interferon-gamma; IFN-gamma;
KM idiopathic pulmonary fibrosis; viral infection; mycobacterial disease;
KM malaria; leishmaniasis; toxoplasmosis; schistosomiasis; clonorchiasis;
KW immunoglobulin E (IgE)-related disorder; antiallergic; antiasthmatic;
KW vincicide; antibacterial; protozoacide; ss.
XX
XX Synthetic.
OS
PN WO200252002-A2.
XX
XX 04-JUL-2002.
PD
PF 27-DEC-2001; 2001WO-US50821.
XX
PR 27-DEC-2000; 2000US-258675P.
XX
PA (DYNAVAX TECHNOLOGIES CORP.
XX Fearon XL, Dina D;
PI WPI, 2002-657426/70.
XX
XX Immunomodulatory polynucleotide for modulating an immune response in a
PT subject suffering from disorders associated with Th2-type immune
PT response, e.g. allergy, or infectious disease, comprises an
PT immunostimulatory sequence -
PS Example 1, Page 71; 95pp; English.
XX
XX The present invention describes an immunomodulatory polynucleotide (I)
CC comprising an immunostimulatory sequence (ISS). Also described: (1) an
CC immunomodulatory composition comprising (1); (2) an immunomodulatory
CC polynucleotide/microcarrier (IMP/MC) complex, comprising (1) linked to a
CC biodegradable MC, where the MC is less than 10 micrometre in size; and
CC (3) a kit comprising (1). (I) has antiallergic, antiasthmatic, virucide,
CC antibacterial and protozoacide activities, and can be used as a modulator
CC of immune response. (I) is useful for modulating an immune response in an
CC individual suffering from disorders associated with a Th2-type immune
CC response, especially an allergy or asthma, or an infectious disease. (I)
CC is also useful for increasing interferon-gamma (IFN-gamma) in an
CC individual having idiopathic pulmonary fibrosis, or IFN-alpha in an
CC individual having a viral infection. (I) is further useful for
CC ameliorating a symptom of an infectious disease caused by a cellular
CC pathogen such as mycobacterial disease, malaria, leishmaniasis,
CC toxoplasmosis, schistosomiasis and clonorchiasis in an individual, or a
CC symptom of an immunoglobulin E (IgE)-related disorder, preferably an
CC allergy-related disorder, in particular asthma in an individual. The
CC present sequence represents an immunomodulatory related oligonucleotide
CC which was used in an example from the present invention.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;

OY Query Match 71.4%; Score 15; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0

DB 6 GAACGTCGAGATGA 20
|||||
8 GAACGTCGAGATGA 22

RESULT 48
AAD24885
AAC AAD24885 standard; DNA; 22 BP.

DT 12-MAR-2002 (first entry)

DE Immunostimulatory oligodeoxynucleotide (ISS-ODN) 1.

XX Cell death; DNA damage; DNA-dependent protein kinase; DNA-PK; necrosis;
 KW immune response; apoptosis; Alzheimer's disease; Parkinson's disease;
 KW rheumatoid arthritis; inflammation; osteoporosis; myocardial infarction;
 KW liver disease; reperfusion injury; carcinoma; multiple sclerosis; stroke;
 KW amyotrophic lateral sclerosis; Acquired Immune Deficiency Syndrome; AIDS;
 KW head injury damage; aplastic anaemia; tumour; organ transplantation;
 KW cerebral infarction; follicular lymphomas; systemic lupus erythematosus;
 KW viral infection; glomerulonephritis; apoptosis; autoimmune disorder;
 KW sepsis; immunostimulatory oligodeoxynucleotide; ISS-ODN; ss.
 XX
 OS Unidentified.
 XX
 PN WO200185910-A2.
 XX
 PD 15-NOV-2001.
 XX
 PF 04-MAY-2001; 2001WO-US14508.
 XX
 PR 05-MAY-2000; 2000US-202274P.
 PR 17-JAN-2001; 2001US-262321P.
 XX
 PA (REGC) UNIV CALIFORNIA.
 PI Raz E, Lois AF, Takabayashi K;
 XX
 DR WPI; 2002-062244/08.
 XX
 PT Modulating cell death or reducing DNA damage in eukaryotic cells,
 PT useful for reducing cell death in individual or organ, comprises
 PT contacting cell with agent modulating biological activity of
 PT DNA-dependent protein kinase -
 PT
 PS Example 1; Page 29; 57pp; English.
 XX
 CC The invention relates to a method for modulating cell death or reducing
 CC DNA damage in an eukaryotic cell by contacting the cell with an agent
 CC that modulates the biological activity of DNA-dependent protein kinase
 CC (DNA-PK). The invention also relates nucleic acids which modulate the
 CC immune response binding to Ku antigen, resulting in activation of DNA-PK.
 CC The method is useful for modulating cell death or reducing DNA damage in
 CC an eukaryotic cell, for treating any disorder resulting from a genotoxic
 CC agent to a cell e.g., necrosis, apoptosis. The method is also useful
 CC for treating cell death-related indications such as Alzheimer's disease,
 CC Parkinson's disease, rheumatoid arthritis, septic shock, sepsis, stroke,
 CC central nervous system inflammation, osteoporosis, degenerative liver
 CC disease, cerebellar degeneration, reperfusion injury, multiple sclerosis,
 CC amyotrophic lateral sclerosis, myocardial infarction, head injury damage,
 CC acquired immunodeficiency syndrome (AIDS), aplastic anaemia, cerebral
 CC infarction, bypass heart surgery, organ transplantation. The method is
 CC also useful for treating follicular lymphomas, carcinomas, autoimmune
 CC disorders (systemic lupus erythematosus), hormone dependent tumours,
 CC immune mediated glomerulonephritis; apoptosis and viral infections. The
 CC present sequence is immunostimulatory oligodeoxynucleotide (ISS-ODN)
 CC used for identifying ISS-binding protein, which is used in the
 CC exemplification of the invention.
 CC
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 XX

Query Match 71.4%; Score 15; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
 |||||
 DB 8 GAACGTCGAGATGA 22

RESULT 49
 AAS16337
 ID AAS16337 standard; DNA; 22 BP.
 XX
 AC AAS16337;

XX
 DT 14-FEB-2002 (first entry)
 XX
 DE ISS polynucleotide #1 useful for treating herpes virus infections.
 XX
 KW Herpes simplex virus; HSV infection; immunostimulatory sequence; ISS;
 KW immune response; alphaherpesvirinae; herpes virus zoster virus; VZV;
 KW HSV-1; HSV-2; chicken pox; herpes labialis; cold sore; genital herpes;
 KW viricide; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT modified_base 1..22
 FT /tag= a
 FT /mod_base= OTHER
 FT /note= "Optionally phosphorothioate internucleotide
 FT linkages"
 XX
 PN WO200168103-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 12-MAR-2001; 2001WO-US07841.
 XX
 PR 10-MAR-2000; 2000US-188556P.
 PR 09-MAR-2001; 2001US-0802518.
 XX
 PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 PI Van Nest G;
 XX
 DR WPI; 2002-041171/05.
 XX
 PT Preventing, reducing the severity or reducing the recurrence of an
 PT infection or symptom of herpes simplex virus (HSV), e.g. HSV-2,
 PT comprises administering an immunostimulatory sequence to an individual
 PT -
 PS Claim 5; Page 41; 49pp; English.
 XX
 CC The present invention relates to novel methods of treating, preventing,
 CC or reducing the severity or recurrence of a symptom of herpes simplex
 CC virus (HSV) infection in an individual who has been exposed to or who is
 CC infected with HSV. The method comprises administering a polynucleotide
 CC having an immunostimulatory sequence (ISS; AAS16337-AAS16345) which
 CC induces an immune response. A composition containing ISS is administered
 CC without a HSV (alphaherpesvirinae) antigen. The composition can be
 CC included in a kit for ameliorating or preventing a symptom of HSV
 CC infection caused by herpes virus zoster virus (VZV), HSV-1 and
 CC particularly HSV-2. Such HSV infections include chicken pox, herpes
 CC labialis (cold sores) and genital herpes. The present sequence represents
 CC one of the ISS polynucleotides of the invention.
 CC Note: The present sequence is shown as single stranded in the
 CC specification, but the patentees state on page 20 that this sequence may
 CC be double stranded.
 CC
 SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 XX

Query Match 71.4%; Score 15; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
 |||||
 DB 8 GAACGTCGAGATGA 22

RESULT 50
 AAS16338
 ID AAS16338 standard; DNA; 22 BP.
 XX
 AC AAS16338;

XX 14-FEB-2002 (first entry)
 XX ISS polynucleotide #2 useful for treating herpes virus infections.
 DE Herpes simplex virus; HSV infection; immunostimulatory sequence; ISS;
 XX immune response; alphaherpesvirinae; herpes virus zoster virus; VZV;
 KW HSV-1; HSV-2; chicken pox; herpes labialis; cold sore; genital herpes;
 KW virucide; ss.
 XX Synthetic.
 OS WO200168103-A2.
 XX 20-SEP-2001.
 XX 12-MAR-2001; 2001WO-US07841.
 PF 10-MAR-2000; 2000US-188556P.
 PR 09-MAR-2001; 2001US-0802518.
 XX (DYNAX-) DYNAVAX TECHNOLOGIES CORP.
 PA Van Nest G;
 PI WPI; 2002-041171/05.
 DR Preventing, reducing the severity or reducing the recurrence of an
 XX infection or symptom of herpes simplex virus (HSV), e.g. HSV-2,
 PT comprises administering an immunostimulatory sequence to an individual
 PT
 XX
 PS Disclosure; Page 19; 49pp; English.
 XX The present invention relates to novel methods of treating, preventing,
 CC or reducing the severity or recurrence of a symptom of herpes simplex
 CC virus (HSV) infection in an individual who has been exposed to or who is
 CC infected with HSV. The method comprises administering a polynucleotide
 CC having an immunostimulatory sequence (ISS; AAS16337-AAS16345) which
 CC induces an immune response. A composition containing ISS is administered
 CC without a HSV (alphaherpesvirinae) antigen. The composition can be
 CC included in a kit for ameliorating or preventing a symptom of HSV
 CC infection caused by herpes virus zoster virus (VZV), HSV-1 and
 CC particularly HSV-2. Such HSV infections include chicken pox, herpes
 CC labialis (cold sore) and genital herpes. The present sequence represents
 CC one of the ISS polynucleotides of the invention.
 CC Note: The present sequence is shown as single stranded in the
 CC specification, but the patentees state on page 20 that this sequence may
 CC be double stranded.
 CC
 SO Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;
 QY Query Match 71.4%; Score 15; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 GAACGTCGAGATGA 20
 DB 8 GAACGTCGAGATGA 22

RESULT 51
 AAS16348
 ID AAS16348 standard; DNA; 22 BP.
 XX AAS16348;
 AC
 XX 14-FEB-2002 (first entry)
 DT
 XX ISS polynucleotide #1 useful for treating papillomavirus infections.
 DE Animal papillomavirus infection; human papillomavirus; HPV; STD; wart;
 KW sexually transmitted disease; cervical cancer; immune response;
 KW

KW immunostimulatory sequence; ISS; virucide; phosphorothioate; ss.
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FH modified_base 1..22
 FT /*tag= a
 FT /mod_base= OTHER
 FT /note= "Optionally phosphorothioate linkages"
 XX
 XX WO200168117-A2.
 XX 20-SEP-2001.
 XX 12-MAR-2001; 2001WO-US07842.
 PF 10-MAR-2000; 2000US-188265P.
 PR 09-MAR-2001; 2001US-0802445.
 XX (DYNAX-) DYNAVAX TECHNOLOGIES CORP.
 PA Van Nest G;
 PI WPI; 2002-041172/05.
 DR Treating, preventing or ameliorating papillomavirus infections,
 XX comprises administering a composition comprising a polynucleotide
 PT having an immunostimulatory sequence to the individual
 PT
 XX Claim 4; Page 39; 44pp; English.
 XX The present invention relates to novel methods of treating, preventing,
 CC or reducing the severity or recurrence of a symptom of papillomavirus
 CC infection in an individual that has been exposed to or who is infected
 CC with papillomavirus. The method comprises administering a polynucleotide
 CC having an immunostimulatory sequence (ISS; AAS16348-AAS16355) which
 CC induces an immune response. A composition containing ISS is administered
 CC without a papillomavirus antigen. The composition can be included in a
 CC kit for ameliorating or preventing a symptom of human or animal
 CC papillomavirus infection. Infections with human papillomavirus (HPV)
 CC which can be prevented or treated using the method of the invention
 CC include sexually transmitted diseases (STDs), warts, papillomas and
 CC cervical cancer. The present sequence represents one of the ISS
 CC polynucleotides of the invention.
 CC Note: The present sequence is shown as single stranded in the
 CC specification, but the patentees state on page 20 that this sequence may
 CC be double stranded.
 CC
 SO Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 QY Query Match 71.4%; Score 15; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 GAACGTCGAGATGA 20
 DB 8 GAACGTCGAGATGA 22

RESULT 52
 AAS16349
 ID AAS16349 standard; DNA; 22 BP.
 XX AAS16349;
 AC
 XX 14-FEB-2002 (first entry)
 DT
 XX ISS polynucleotide #2 useful for treating papillomavirus infections.
 DE Animal papillomavirus infection; human papillomavirus; HPV; STD; wart;
 KW sexually transmitted disease; cervical cancer; immune response;
 KW immunostimulatory sequence; ISS; virucide; ss.
 KW

```

OS Synthetic.
XX WO200168117-A2.
XX
XX 20-SEP-2001.
XX
XX 12-MAR-2001; 2001WO-US07842.
XX
XX 10-MAR-2000; 2000US-188265P.
XX
XX 09-MAR-2001; 2001US-0802445.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Van Nest G;
XX
XX WPI; 2002-041172/05.
XX
XX
XX Treating, preventing or ameliorating papillomavirus infections,
XX comprising administering a composition comprising a polynucleotide
XX having an immunostimulatory sequence to the individual.
XX
XX Disclosure; Page 19; 44pp; English.
XX
XX The present invention relates to novel methods of treating, preventing,
XX or reducing the severity or recurrence of a symptom of papillomavirus
XX infection in an individual that has been exposed to or who is infected
XX with papillomavirus. The method comprises administering a polynucleotide
XX having an immunostimulatory sequence (ISS; AAS16348-AAS16355) which
XX induces an immune response. A composition containing ISS is administered
XX without a papillomavirus antigen. The composition can be included in a
XX kit for ameliorating or preventing a symptom of human or animal
XX papillomavirus infection. Infections with human papillomavirus (HPV)
XX which can be prevented or treated using the method of the invention
XX include sexually transmitted diseases (STDs), warts, papillomas and
XX cervical cancer. The present sequence represents one of the ISS
XX polynucleotides of the invention.
XX Note: The present sequence is shown as single stranded in the
XX specification, but the patentees state on page 20 that this sequence may
XX be double stranded.
XX
XX Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 6 GAACGTCGAGATGA 20
XX |||||
XX 8 GAACGTCGAGATGA 22
XX
XX Db
XX
XX RESULT 53
XX AAD21877
XX ID AAD21877 standard; DNA; 22 BP.
XX
XX AC AAD21877;
XX
XX DT 12-FEB-2002 (first entry)
XX
XX DE Immunostimulatory sequence oligonucleotide (ISS-ODN) #1.
XX
XX CYC cytotoxic T lymphocyte; CTL; T cell; tumour load; cancer radiotherapy;
XX immunostimulatory sequence oligonucleotide; ISS-ODN; chemotherapy;
XX immunosuppression; transplantation; autoimmune disease; infection;
XX acquired immune deficiency syndrome; AIDS; intracellular pathogen;
XX cytomegalovirus; mycobacterial infection; Epstein-Barr virus;
XX varicella zoster virus; human immunodeficiency virus; HIV;
XX phosphorothioate backbone; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
XX modified_base 1..22
XX

```

```

FT /*tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
FT
FT modified_base 1
FT /*tag= b
FT /mod_base= OTHER
FT /note= "Disulphide thymine"
FT
XX WO200172123-A1.
XX
XX 04-OCT-2001.
XX
XX 28-MAR-2001; 2001WO-US10118.
XX
XX 28-MAR-2000; 2000US-192537P.
XX
XX 11-MAY-2000; 2000US-203567P.
XX
XX 05-JUL-2000; 2000US-215895P.
XX
XX (RSCC) UNIV CALIFORNIA.
XX (VETE-) DEPT VETERANS AFFAIRS.
XX
XX Raz E, Cho HJ, Richman DD, Horner AA;
XX
XX WPI; 2002-010699/01.
XX
XX Increasing antigen-specific cytotoxic T lymphocyte activity in a CD4+ T
XX cell deficient individual, useful to treat immunodeficiency and block
XX HIV infection, comprises administering immunostimulatory nucleic acid
XX
XX Example 1; Page 44; 91pp; English.
XX
XX The present invention relates to a method for increasing antigen-specific
XX cytotoxic T lymphocyte (CTL) activity in a CD4+ T cell-deficient
XX individual, comprising administering an immunostimulatory sequence
XX oligonucleotide (ISS-ODN). The immunostimulatory nucleic acids of the
XX invention are used in CD4+ T cell-deficient individuals to decrease
XX tumour load, to treat a primary or acquired immunodeficiency, and
XX particularly where the acquired immunodeficiency is temporary and due
XX to cancer radiotherapy or chemotherapy or immunosuppression following
XX bone marrow or organ transplantation, or autoimmune disease treatment,
XX or is acquired immunodeficiency syndrome (AIDS). The nucleic acids may
XX be used to treat a person at risk of becoming CD4+ T cell-deficient,
XX particularly where someone at risk of cancer recurrence. They are also
XX used to treat infection, particularly by an intracellular pathogen,
XX especially one caused by cytomegalovirus, Mycobacterium tuberculosis,
XX M. avium, Epstein-Barr virus, a fungus yeast, varicella zoster virus or
XX human immunodeficiency virus (HIV). The present sequence is a 5'
XX disulfide-linked phosphorothioate immunostimulatory sequence
XX oligonucleotide (ISS-ODN), used in the exemplification of the invention.
XX
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
XX
XX Query Match 71.4%; Score 15; DB 24; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 19;
XX Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Oy 6 GAACGTCGAGATGA 20
XX |||||
XX 8 GAACGTCGAGATGA 22
XX
XX Db
XX
XX RESULT 54
XX ABA03833
XX ID ABA03833 standard; DNA; 22 BP.
XX
XX AC ABA03833;
XX
XX DT 12-FEB-2002 (first entry)
XX
XX DE Immunostimulatory sequence (ISS) SEQ ID NO:1.
XX
XX Immunomodulatory polynucleotide/microcarrier complex; IMP/MC; IGB;
XX

```

KM immunomodulation; immunostimulation; phosphorothioate; immunomodulator
 KM antiallergic; antibacterial; antiprotocoral; antihypertensive; hepatotropic
 KM nephrotropic; interferon-alpha stimulator; interferon-gamma stimulator;
 KM immunoglobulin B stimulator; immune response; IP; scleroderma; malaria
 KM idiopathic pulmonary fibrosis; cutaneous radiation-induced fibrosis;
 KM hepatic fibrosis; renal fibrosis; infectious disease; leiomyomatosis;
 KM mycobacterial disease; toxoplasmosis; schistosomiasis;
 KM allergy; allergy-induced asthma; prophylactic vaccine; cancer; ss.
 XS
 XS Synthetic.

	RESULT	55
ABAO03834	ID	ABAO03834 standard; DNA; 22 BP.
XX		
XX		
AC	ABAO03834;	
XX		
DT	12-FEB-2002	(first entry)
XX		
DE	Immunostimulatory sequence (ISS)	SEQ ID NO:2
XX		

FH	Key	Location/Qualifiers
FT	modified_base	1..22
PT		/*tag= a
FT		/mod_base= OTHER
PT		/note= "phosphorochioate linkages"
XX		
XX		
PN	WO200168144-A2.	
PD	20-SEP-2001.	

allergy; allergy-induced asthma; propylactic vaccine; cancer; ss. immunomodulatory polynucleotide/microcarrier complex; IMF/MC; IgE; immunomodulation; immunostimulation; phosphorothiate; immunomodulator; anti-allergic; antibacterial; antiprotocozal; antiparasitic; hepatotropic; interferon-alpha stimulator; interferon-gamma stimulator; immunoglobulin E stimulator; immune response; IPF; scleroderma; malarial; idiopathic pulmonary fibrosis; cutaneous radiation-induced fibrosis; hepatic fibrosis; renal fibrosis; infectious disease; leishmaniasis; mycobacterial disease; toxoplasmosis; schistosomiasis; chlororchiasis

PF 12-MAR-2001; 2001WO-US07848.
XX
XX 10-MAR-2000; 2000US-188303P.
PR 09-MAR-2001; 2001US-0802359.
XX
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP
XX
PI Van Nest G, Tuck S;
XX
XX WPI; 2002-049002/06.
XX
XX

Synthetic.
MO200168144-A2.
20-SEP-2001.
12-MAR-2001; 2001WO-US07848.
10-MAR-2000; 2000US-188303P.
09-MAR-2001; 2001US-0802359.

PT New immunomodulatory polynucleotide/microcarrier complex, useful for modulating the immune response of individuals, particularly humans, or for treating idiopathic pulmonary fibrosis, scleroderma, malaria or allergies -

(DYNA-) DYNAVAX TECHNOLOGIES CORP.
Van Nest G, Tuck S;
MPI; 2002-049002/06.

PS Claim 14; Page 49; 63pp; English

New immunomodulatory

The present invention describes an immunomodulatory polynucleotide/microcarrier (IMP/MC) complex (I), which comprises a polynucleotide having an immunostimulatory sequence (ISS) linked to a biodegradable microcarrier (MC). The ISS comprises the sequence: 5'-CG-3', where the MC is less than 10 microm in size. (I) has immunomodulator, antiallergic, antibacterial, antiprotosol, antiparasitic, hepatotropic and nephrotropic activities. It can be used as an interferon (IFN)-alpha stimulator, IFN-gamma stimulator or an immunoglobulin E (IgE) stimulator (I) can be used for modulating the immune response of individuals, particularly humans. The IMP/MC complex is particularly useful for treating idiopathic pulmonary fibrosis (IPF), scleroderma, cutaneous radiation-induced fibrosis, hepatic fibrosis including schistosomiasis-induced hepatic fibrosis, renal fibrosis, infectious diseases caused by cellular pathogen (e.g. a mycobacterial disease, malaria, leishmaniasis, toxoplasmosis, schistosomiasis or chlamydiae), or disorders associated with a Th2-type immune response (e.g. allergies or allergy-induced asthma). The IMP/MC may also be used in individuals receiving therapeutic or prophylactic vaccines, in individuals suffering from cancer, or in individuals at risk of exposure to an infectious agent. The present sequence represents a specifically claimed ISS which can be used in an IMP/MC complex of the present invention.

SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
Query Match 71.4%; Score 15; DB 24; Length 22;

CC vaccines, in individuals suffering from cancer or in individuals at
CC risk of exposure to an infectious agent. The present sequence represents
CC an ISS given in the exemplification of the present invention.

Qy	6	GAACGTCGAGATGA	20
Db	8	GAACGTCGAGATGA	22

Query Match	71.4%
Best Local Similarity	100.0%
Matches	15; Conservative

Db 8 GAACGTCGAGATGA 22

RESULT 56

ABA03844 ID ABA03844 standard; DNA; 22 BP.

AC ABA03844;

DT 12-FEB-2002 (first entry)

DE Immunostimulatory sequence (ISS) SEQ ID NO:1.

XX Immunostimulatory sequence; ISS; immunostimulation; viral infection;
KW immunomodulation; virucide; gene therapy; viraemia; phosphorothioate; ss.

OS Synthetic.

XX Key Location/Qualifiers

FT modified_base 1..22

FT /*tag= a

FT /mod_base= OTHER

FT /note= "phosphorothioate linkages"

PN WO200168077-A2.

PD 20-SEP-2001.

PP 12-MAR-2001; 2001WO-US07840.

PR 10-MAR-2000; 2000US-188302P.

PR 09-MAR-2001; 2001US-0802685.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Van Nest G;

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

RESULT 57 ABA03845 ID ABA03845 standard; DNA; 22 BP.

AC ABA03845;

DT 12-FEB-2002 (first entry)

DE Immunostimulatory sequence (ISS) SEQ ID NO:2.

XX Immunostimulatory sequence; ISS; immunostimulation; viral infection;
KW immunomodulation; virucide; gene therapy; viraemia; ss.

OS Synthetic.

PN WO200168077-A2.

PD 20-SEP-2001.

PP 12-MAR-2001; 2001WO-US07840.

PR 10-MAR-2000; 2000US-188302P.

PR 09-MAR-2001; 2001US-0802685.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Van Nest G;

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

RESULT 58 ABA03856 ID ABA03856 standard; DNA; 22 BP.

AC ABA03856;

DT 12-FEB-2002 (first entry)

DE Immunostimulatory sequence (ISS) SEQ ID NO:1.

XX Immunostimulatory sequence; ISS; immunostimulation; viral infection;
KW immunomodulation; virucide; gene therapy; viraemia; ss.

OS Synthetic.

PN WO200168077-A2.

PD 20-SEP-2001.

PP 12-MAR-2001; 2001WO-US07840.

PR 10-MAR-2000; 2000US-188302P.

PR 09-MAR-2001; 2001US-0802685.

XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.

XX Van Nest G;

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

XX WPI; 2002-048999/06.

KM Immunostimulatory sequence; ISS; immunomodulation; HBV; HCV; infection;
KM hepatitis B virus; hepatitis C virus; virucide; anti-inflammatory;
KM hepatotropic; gene therapy; hepatitis infection; viraemia; jaundice;
KM fatigue; abdominal pain; portal hypertension; cirrhosis;
KM phosphorochioate; ss.
XX
XX Synthetic.
OS
FH Key location/Qualifiers
FT modified_base 1..22
FT /*tag= a
FT /mod_base= OTHER
FT /note= "phosphorochioate linkages"
XX
XX WO200168078-A2.
XX
XX 20-SEP-2001.
XX
XX 12-MAR-2001; 2001WO-US07931.
XX
XX 10-MAR-2000; 2000US-188301P.
PR 09-MAR-2001; 2001US-0802370.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Van Nest G;
XX
XX WPI; 2002-049000/06.
XX
XX
XX Reducing viremia and blood levels of hepatitis virus antigen in an
PT individual infected with hepatitis B virus, comprises administering a
PT composition comprising a polynucleotide having an immunostimulatory
PT sequence -
XX
XX
XX Claim 5; Page 38; 43pp; English.
XX
XX The present invention describes a method for reducing viraemia or blood
CC levels of a hepatitis virus antigen in an individual infected with
CC hepatitis B virus (HBV). The method comprises administering a composition
CC comprising a polynucleotide having an immunostimulatory sequence (ISS)
CC to the individual, where the ISS comprises the sequence 5'-C, G-3', an
CC HBV antigen is not administered in conjunction with administration of
CC the composition, and where the composition is administered in an amount
CC sufficient to reduce HBV viraemia or blood levels of a hepatitis virus
CC antigen. ISS has virucide, anti-inflammatory and hepatotropic activities,
CC and can be used in gene therapy. The method can be used for suppressing
CC and/or ameliorating hepatitis infection in an individual, especially for
CC preventing, palliating, ameliorating, reducing and/or eliminating one or
CC more symptoms of HBV or HCV (hepatitis C virus) infection without
CC administering HBV or HCV antigens. The method is specifically useful for
CC reducing viraemia and hepatitis viral antigen in blood. ISS-containing
CC polynucleotides may also be used to improve physical symptoms such as
CC jaundice, fatigue, abdominal pain, and other clinical/laboratory
CC findings associated with hepatitis such as blood levels of liver enzymes,
CC portal hypertension, or cirrhosis. The present sequence represents a
CC specifically claimed ISS oligonucleotide for use in the method of the
CC invention.
XX
XX
SQ Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
Query Match 71.4%; Score 15; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||
Db 8 GAACGTTGAGATGA 22

RESULT 59
ABA03857 standard; DNA; 22 BP.
XX

AC ABA03857;
XX
XX 12-FEB-2002 (first entry)
XX
XX Immunostimulatory sequence (ISS) SEQ ID NO:2.
DE
XX
XX Immunostimulatory sequence; ISS; immunomodulation; HBV; HCV; infection;
KM hepatitis B virus; hepatitis C virus; virucide; anti-inflammatory;
KM hepatotropic; gene therapy; hepatitis infection; viraemia; jaundice;
KM fatigue; abdominal pain; portal hypertension; cirrhosis; ss.
XX
XX Synthetic.
OS
XX
XX WO200168078-A2.
XX
XX 20-SEP-2001.
XX
XX 12-MAR-2001; 2001WO-US07931.
XX
XX 10-MAR-2000; 2000US-188301P.
PR 09-MAR-2001; 2001US-0802370.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX
XX Van Nest G;
XX
XX WPI; 2002-049000/06.
XX
XX
XX Reducing viremia and blood levels of hepatitis virus antigen in an
PT individual infected with hepatitis B virus, comprises administering a
PT composition comprising a polynucleotide having an immunostimulatory
PT sequence -
XX
XX
XX Disclosure; Page 20; 43pp; English.
XX
XX The present invention describes a method for reducing viraemia or blood
CC levels of a hepatitis virus antigen in an individual infected with
CC hepatitis B virus (HBV). The method comprises administering a composition
CC comprising a polynucleotide having an immunostimulatory sequence (ISS)
CC to the individual, where the ISS comprises the sequence 5'-C, G-3', an
CC HBV antigen is not administered in conjunction with administration of
CC the composition, and where the composition is administered in an amount
CC sufficient to reduce HBV viraemia or blood levels of a hepatitis virus
CC antigen. ISS has virucide, anti-inflammatory and hepatotropic activities,
CC and can be used in gene therapy. The method can be used for suppressing
CC and/or ameliorating hepatitis infection in an individual, especially for
CC preventing, palliating, ameliorating, reducing and/or eliminating one or
CC more symptoms of HBV or HCV (hepatitis C virus) infection without
CC administering HBV or HCV antigens. The method is specifically useful for
CC reducing viraemia and hepatitis viral antigen in blood. ISS-containing
CC polynucleotides may also be used to improve physical symptoms such as
CC jaundice, fatigue, abdominal pain, and other clinical/laboratory
CC findings associated with hepatitis such as blood levels of liver enzymes,
CC portal hypertension, or cirrhosis. The present sequence represents an
CC ISS oligonucleotide given in the exemplification of the present
CC invention.
XX
XX
SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;
Query Match 71.4%; Score 15; DB 24; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||
Db 8 GAACGTTGAGATGA 22

RESULT 60
AAS15592 standard; DNA; 22 BP.
XX
XX AAS15592;
AC

XX 29-JAN-2002 (first entry)
 XX Immunostimulatory oligonucleotide (ISS-ODN) #1.
 DE Immunostimulatory oligonucleotide (ISS-ODN) #1.
 XX Immunostimulatory oligonucleotide; ISS-ODN; anti-allergic; antibacterial;
 KM virucide; fungicide; vaccine; immunogen; plant allergen; rawseed;
 KM grass pollen; food; latex; cat dander; cockroach; house dust mite;
 KM pathogenic parasite; ss.
 XX Synthetic.
 OS
 XX WO200176642-A1.
 PN 18-OCT-2001.
 XX 06-APR-2001; 2001WO-US11290.
 PD 07-APR-2000; 2000US-195890P.
 XX 07-APR-2000; 2000US-195890P.
 PR (REGC) UNIV CALIFORNIA.
 XX
 PA Raz E, Takabayashi K, Nguyen M;
 PI WPI; 2002-025886/03.
 XX
 DR New polynucleotide vaccine for eliciting immune response to an antigen
 XX derived from a pathogen, plant or food, comprises antigen-encoding
 PT nucleic acid sequence derived from non-host species of first phylum or
 PT kingdom -
 XX
 PS Example 4; Page 43; 64pp; English.
 XX
 XX The invention relates to a polynucleotide vaccine (I) comprising a
 CC nucleic acid sequence encoding an antigen derived from a non-host species
 CC of a first phylum or first kingdom, where the nucleic acid sequence
 CC encoding the antigen is modified by deletion of a native signal sequence,
 CC and/or an immunomodulatory nucleic acid sequence. (I) is useful for
 CC modulating an immune response to an antigen, especially a plant (ragweed
 CC or grass pollen), food, latex, cat dander, cockroach, or house dust mite
 CC allergen. (I) is also useful for eliciting an immune response to an
 CC antigen derived from a pathogen, such as bacterium, virus or a parasite.
 CC The vaccine is co-administered with an immunostimulatory nucleotide.
 CC sequence which comprises an unmethylated 5'-CG-3' nucleotide sequence.
 CC Antigens of pathogenic parasites include Plasmodium, Leishmania, fungal,
 CC yeast or other pathogens. The present sequence represents
 CC immunostimulatory oligonucleotide (ISS-ODN) #1 which is co-injected
 CC with (I) to amplify the immune response to the co-administered allergen.
 CC
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 SQ
 Query Match 71.4%; Score 15; DB 24; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 GAACGTCGAGATGA 20
 DB 8 GAACGTCGAGATGA 22
 RESULT 61
 ID AB277582 standard; DNA; 22 BP.
 AC AB277582;
 XX
 DT 03-JUN-2003 (first entry)
 XX
 DE Nucleotide sequence of a control immunostimulatory oligonucleotide.
 XX
 KM Immunomodulatory composition; immune response; Th2-type immune response;
 KM allergy; asthma; infectious disease; vaccine; cancer; IFN-alpha;
 KM IFN-gamma; idiopathic pulmonary fibrosis; scleroderma;

KM cutaneous radiation-induced fibrosis; hepatic fibrosis; renal fibrosis;
 KM viral infection; mycobacterial disease; malaria; leishmaniasis;
 KM toxoplasmosis; schistosomiasis; clonorchiasis; ss.
 OS Synthetic.
 XX WO2003014316-A2.
 PN 20-FEB-2003.
 XX
 PD 07-AUG-2002; 2002WO-US25123.
 PF
 XX 07-AUG-2001; 2001US-310743P.
 PR 25-OCT-2001; 2001US-335263P.
 XX
 XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
 PA Fearon KL, Dina D;
 PI WPI; 2003-248016/25.
 XX
 DR Immunomodulatory composition for modulating immune response and
 XX reducing levels of immunoglobulin E in an individual having the related
 PT disorder, has a complex of microcarrier and an immunomodulatory
 PT oligonucleotide -
 XX
 PS Example 3; Page 62; 79pp; English.
 XX
 XX The specification describes an immunomodulatory composition, which
 CC comprises a complex of a microcarrier and an immunomodulatory
 CC oligonucleotide which is three to six nucleotides in length and which
 CC does not have a sequence selected from 5'-GACGT-3', 5'-TCCGA-3', and
 CC 5'-GAGCT-3'. The composition is useful for modulating an immune
 CC response in an individual suffering from a disorder associated with a
 CC Th2-type immune response which is selected from allergies and
 CC allergy-induced asthma, asthma or infectious disease. The individual
 CC receives a prophylactic or therapeutic vaccine, where the therapeutic
 CC vaccine is selected from an epitope which is selected from an allergy
 CC epitope, a mycobacterial epitope, and a tumour-associated epitope. The
 CC individual is at a risk of exposure to an infectious agent or at risk
 CC of developing cancer, or suffers from cancer or an infectious disease.
 CC The composition is useful for increasing interferon (IFN)-gamma or
 CC IFN-alpha in an individual, where the individual suffers from a disorder
 CC selected from idiopathic pulmonary fibrosis, scleroderma, cutaneous
 CC radiation-induced fibrosis, hepatic fibrosis, and renal fibrosis, viral
 CC infections and cancer. The composition is also useful for ameliorating
 CC one or more symptoms of an infectious disease in an individual, where
 CC the infectious disease is caused by a cellular pathogen. The infectious
 CC disease is selected from mycobacterial disease, malaria, leishmaniasis,
 CC toxoplasmosis, schistosomiasis, and clonorchiasis. The present sequence
 CC represents an immunostimulatory oligonucleotide, used as a control in
 CC the course of the invention.
 CC
 XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
 SQ
 Query Match 71.4%; Score 15; DB 25; Length 22;
 Best Local Similarity 100.0%; Pred. No. 19;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 6 GAACGTCGAGATGA 20
 DB 8 GAACGTCGAGATGA 22
 RESULT 62
 ID AAL51531 standard; DNA; 22 BP.
 AC AAL51531;
 XX
 DT 10-APR-2003 (first entry)
 XX
 DE CTL recognition antigen-related oligonucleotide, SEQ ID No 5.

XX Cytotoxic T-lymphocyte recognition antigen; CTL recognition antigen;
KW human T-lymphocytic leukemia virus-1; HTLV-1; tumour; health food;
KW immune response-inducible vaccine; ds; primer; probe.
XX Unidentified.
XX WO200290981-A1.
XX 14-NOV-2002.
XX 02-MAY-2002; 2002WO-JP04406.
XX 08-MAY-2001; 2001JP-0137526.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX Hanabuchi S, Ohashi T, Kannagi M;
XX WPI; 2003-140232/13.
XX Screening of cytotoxic T-lymphocyte-recognition antigen with a human
PT T-lymphocytic leukemia virus-1 (HTLV-1) antitumor effect, for use as
PT a vaccine, comprises administering a test substance to a
PT HTLV-1-associated disease animal model -
XX Example 10; Page 29; 53pp; Japanese.
XX The invention comprises a method for screening a cytotoxic T-lymphocyte
CC (CTL) recognition antigen, which includes CTLs with antitumor effect
CC against human T-lymphocytic leukemia virus-1 (HTLV-1) tumours. The
CC CTL-recognition antigens identified by the method of the invention are
CC useful as immune response-inducible vaccines, and as components of drug
CC preparations and health foods. The present DNA sequence represents an
CC oligonucleotide that was used in an example of the invention.
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ
Query Match 71.4%; Score 15; DB 25; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22
RESULT 63
AB257964
ID AB257964 standard; DNA; 22 BP.
XX
AC AB257964;
XX
DT 14-APR-2003 (first entry)
XX
DE Immunostimulatory oligodeoxynucleotide ISS-ODN 1018.
XX
KW ISS-ODN 1018; immunostimulant; vaccine; adjuvant; phosphorothioate;
KW gene therapy; liposome; ss.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FT modified_base 1..22
FT /*tag= a
FT /mod_base= "OTHER"
FT /note= "phosphorothioate linkage"
XX
XX WO2003000232-A2.
XX
XX 03-JAN-2003.
XX
XX 25-JUN-2002; 2002WO-IL00507.

XX 25-JUN-2001; 2001US-300072P.
PR 17-DEC-2001; 2001US-339785P.
XX
XX (YISS) YISSUM RES DEV CO HEBREW UNIV JERUSALEM.
XX (REGC) UNIV CALIFORNIA.
XX
PI Barenholz Y, Kedari E, Louria-Hayon Y, Joseph A, Raz E;
PI Takabayashi K;
XX WPI; 2003-201371/19.
XX
XX Loading immunostimulatory oligodeoxynucleotides (ISS-ODNs) in liposomes
PT useful for stimulating an immune response comprises solubilizing at
PT least one liposome-forming lipid in a solvent and drying or
PT freeze-drying the solution -
XX Example; Page 19; 68pp; English.
XX
XX The present sequence is that of phosphorothioate immunostimulatory
CC oligodeoxynucleotide (ISS-ODN) 1018. The invention provides a
CC novel, fast and simple method of preparing liposomes efficiently
CC loaded (i.e. at least 60% loading) with ISS-ODN. The method is
CC based on drying a suspension of amphipathic material and then
CC hydrating it with an aqueous solution containing the ISS-ODN,
CC thereby entrapping it in liposomes formed from the lipid. The
CC ISS-ODN is preferably an endotoxin-free ISS-ODN with a
CC phosphorothioate or phosphodiester backbone. Liposomal ISS-ODN can
CC be used e.g. as a vaccine adjuvant against pathogens and cancer, in
CC the treatment or prevention of diseases caused by certain infectious
CC microorganisms, in the treatment or prevention of allergic
CC diseases, or to boost innate immunity. In examples of the
CC invention, ISS-ODN 1018 was encapsulated in large multilamellar
CC liposomes with up to 95% efficiency. The liposomal formulation was
CC a considerably more potent parenteral adjuvant in mice than the
CC soluble form of ISS-ODN, as shown in experiments with an influenza
CC vaccine. Enhancement of the systemic humoral and cellular response
CC was demonstrated by liposomal ISS-ODN 1018 co-administered with
CC hepatitis B vaccine, and of the systemic humoral response when
CC administered with tuberculosis vaccine. Liposomal ISS-ODN 1018 was
CC also used as an adjuvant for a cancer (murine mammary carcinoma)
CC vaccine, and activated resistance to Leishmaniasis when administered
CC after infection.
XX Sequence 22 BP; 6 A; 3 C; 7 G; 6 T; 0 other;
SQ
Query Match 71.4%; Score 15; DB 25; Length 22;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22
RESULT 64
AAV80098/C
ID AAV80098 standard; DNA; 23 BP.
XX
AC AAV80098;
XX
DT 12-MAR-1999 (first entry)
XX
DE Immunomodulatory oligo comprising an ISS sequence.
XX
XX Immunomodulatory; immunostimulatory; octanucleotide; immune regulation;
KW ISS; cancer; allergy; asthma; hepatitis B infection; papillomavirus;
KW human immunodeficiency virus; influenza; herpes; M. tuberculosis; ss;
KW B. pertussis; malaria; plasmodia; Leishmania; Trypanosoma; Schistosoma.
XX
XX Synthetic.
XX
XX WO9855495-A2.

XX 10-DEC-1998.
PD
XX 05-JUN-1998; 98WO-US11578.
PF
XX 06-JUN-1997; 97US-0048793.
PR
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
PA
XX Dina D, Roman M, Schwartz D;
PI
XX WPI; 1999-059898/05.
DR
XX Immunostimulatory oligonucleotides regulate the immune system - and
PT contain an immune-stimulating octanucleotide sequence; for treating
PT cancer, allergic and infectious diseases
XX
PS Claim 6; Page 29; 63pp; English.
XX
XX The invention relates to immunomodulatory oligonucleotides that comprise
CC at least 1 immunostimulatory octanucleotide sequence (ISS) where the ISS
CC sequences are selected from the group consisting of AACGTTCC, AACGTTCC,
CC GAGGTTCC, and GAGGTTCC. The immunomodulatory sequences are used to treat
CC patients needing immune regulation, such as those suffering from cancer,
CC an allergic disease and asthma. They are also used to prevent infectious
CC diseases such as influenza, herpes, hepatitis B, human immunodeficiency
CC and papillomavirus, Hemophilus influenza, Mycobacterium tuberculosis and
CC Bordetella pertussis, malarial plasmodia, Leishmania, Trypanosoma and
CC Schistosoma. The immunomodulatory sequences are used to screen for human
CC immunostimulatory activity by incubating macrophage cells and the
CC oligonucleotide; and determining the relative amount of Th1-biased
CC cytokines in the supernatant. Sequences AAV80096 to AAV80103 represent
CC specific claimed examples of such immunomodulatory oligonucleotides.
XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;
Query Match 71.4%; Score 15; DB 20; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTTGAGATGA 20
DB 15 GAACGTTGAGATGA 1
RESULT 65
AAA38067/C
ID AAA38067 standard; DNA; 23 BP.
AC
XX AAA38067;
XX
XX 24-AUG-2000 (first entry)
DT
XX Immunostimulatory sequence (ISS) #3.
DE
XX Immunostimulatory sequence; ISS; immunomodulator; glycoprotein 120;
KW gp120; human immunodeficiency virus; HIV; immune response; infection;
KW development; ss.
XX
XX Synthetic.
OS
XX WO200021556-A1.
XX
XX 20-APR-2000.
PD
XX 08-OCT-1999; 99WO-US23677.
PF
XX 09-OCT-1998; 98US-0103733.
PR
XX 07-OCT-1999; 99US-0415186.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
PA
XX Tighe H, Raz E, Schwartz D, Takabayashi K;
PI

XX WPI; 2000-317846/27.
DR
XX Anti-HIV composition comprises immunostimulatory polynucleotides and
PT HIV glycoprotein gp120 useful for modulating, stimulating an immune
PT response against HIV in an HIV infected individual -
XX
XX Disclosure; Page 16; 65pp; English.
XX
XX The present invention relates to an immunostimulatory composition
CC comprising a human immunodeficiency virus (HIV) antigen, and an
CC immunomodulatory polynucleotide comprising an immunostimulatory sequence
CC (ISS). This sequence represents an ISS that can be used in the
CC composition. An immunostimulatory composition which comprises a gp120
CC conjugated to it and not conjugated, is used for modulating or
CC stimulating a specific immune response against gp120 in an individual by
CC producing anti-gp120 antibodies or gp120 specific cytotoxic T cells. It
CC is also used for suppressing or delaying development of HIV infection in
CC an individual infected with HIV or an individual at risk of infection
CC with HIV, respectively. It is also used for treating an individual
CC infected with HIV in need of immune modulation.
XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;
Query Match 71.4%; Score 15; DB 21; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTTGAGATGA 20
DB 15 GAACGTTGAGATGA 1
RESULT 66
AAS14666/C
ID AAS14666 standard; DNA; 23 BP.
AC
XX AAS14666;
XX
XX 18-DEC-2001 (first entry)
DT
XX Immunostimulatory sequence, ISS #3.
DE
XX Immunostimulatory sequence; ISS; ds; antiviral; immunogen;
KW respiratory syncytial virus; RSV; influenza virus; rhinovirus;
KW adenovirus; measles virus; mumps virus; parainfluenza virus;
KW rubella virus; poxvirus; parvovirus; hantavirus; varicella virus.
XX
XX Respiratory syncytial virus.
OS
XX Synthetic.
OS
XX WO200168116-A2.
XX
XX 20-SEP-2001.
PD
XX 12-MAR-2001; 2001WO-US07839.
PF
XX 10-MAR-2000; 2000US-188583P.
PR
XX 09-MAR-2001; 2001US-0802686.
XX
XX (DYNA-) DYNAVAX TECHNOLOGIES CORP.
PA
XX Van Nest G;
PI
XX WPI; 2001-607438/69.
DR
XX Suppressing a respiratory syncytial virus infection by administering an
PT immunostimulatory sequence at the site of infection is useful to
PT prevent and treat lower respiratory tract viral infections -
XX
XX Disclosure; Page 15; 40pp; English.
PS
XX

CC The invention relates to suppressing a respiratory syncytial virus (RSV) infection in an exposed individual, comprising administering a polynucleotide comprising an immunostimulatory sequence (ISS) comprising the sequence 5'-C, G-3', where an RSV antigen is not administered.

CC The invention is used to prevent and treat respiratory syncytial virus infection of the lower respiratory tract and other viruses including influenza virus, rhinovirus, adenovirus, measles virus, mumps virus, parainfluenza virus, rubella virus, poxvirus, parvovirus, the administration is also included. Unlike the prior art antiviral agent ribavirin, which is a potential teratogen, the invention provides a treatment which does not carry unacceptable side effects. Other prior art medications treat the symptoms only, whilst the invention treats the infection. The present sequence is an ISS of the invention.

CC Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTGAGATGA 20
Db 15 GAACGTTGAGATGA 1

RESULT 67
AAH75994/C
ID AAH75994 standard; DNA; 23 BP.
AC AAH75994;
XX
DT 15-NOV-2001 (first entry)
XX
DE Immunomodulatory oligonucleotide #3.
XX
KW Immunomodulatory; immunostimulatory; Th1-type immune response;
KW Th2-type immune response; interferon; idiopathic pulmonary fibrosis;
KW viral infection; ss.
XX
OS Synthetic.
XX
PN WO200168143-A2.
XX
PD 20-SEP-2001.
XX
PF 12-MAR-2001; 2001WO-US07843.
XX
PR 10-MAR-2000; 2000US-0188557.
PR 09-MAR-2001; 2001US-0802376.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
PI Van Nest G, Tuck S;
PI WPI; 2001-582389/65.
XX
DR
XX Immunomodulatory polynucleotide/microcarrier complexes comprise an immunostimulatory sequence containing polynucleotide linked to a nonbiodegradable microcarrier -
PT nonbiodegradable microcarrier
XX
PS Disclosure; Page 18; 61pp; English.
XX
CC The present invention relates to immunomodulatory polynucleotide/microcarrier complexes. The complexes comprise an immunostimulatory sequence (ISS), e.g. the present sequence, linked to a nonbiodegradable microcarrier provided that if the microcarrier is gold, latex or magnetic then the linkage is not biotin/avidin. The complex is useful for modulating an immune response (especially stimulating a Th1-type response or suppressing a Th2-type response), increasing interferon-gamma (especially in a patient suffering from idiopathic pulmonary fibrosis), increasing interferon-alpha (especially in patients suffering from viral infection) and reducing levels of IgE.

XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTGAGATGA 20
Db 15 GAACGTTGAGATGA 1

RESULT 68
AAH41575/C
ID AAH41575 standard; DNA; 23 BP.
AC AAH41575;
XX
DT 24-AUG-2001 (first entry)
XX
DE Immunostimulatory sequence (ISS) SEQ ID NO:3.
XX
KW Immunostimulatory sequence; ISS; immunomodulatory; immune response;
KW antigen; anti-allergic; modulation; Th1 lymphocyte stimulation; allergy;
KW Th1-associated cytokine; Th2 lymphocyte suppression; cytokine; ss.
XX
OS Synthetic.
XX
PN WO200135991-A2.
XX
PD 25-MAY-2001.
XX
PF 15-NOV-2000; 2000WO-US31385.
XX
PR 15-NOV-1999; 99US-0165467.
PR 14-NOV-2000; 2000US-0713136.
XX
PA (DYNA-) DYNAVAX TECHNOLOGIES CORP.
PI Tuck S, Van Nest G;
PI WPI; 2001-329209/34.
XX
DR
XX Populations of conjugate molecules comprising polynucleotide
PT Immunostimulatory sequences polynucleotides and antigens, useful for
PT controlling immune responses -
XX
PS Disclosure; Page 30; 97pp; English.
XX
CC The present invention describes immunomodulatory populations (I) and (II) of conjugate molecules (Cm) comprising immunostimulatory sequences (ISS) of polynucleotides and antigens. The extent of conjugation affects the immunological properties (e.g. the extent of antigen-specific antibody formation, including Th1-associated antibody formation) so the conjugates are used for altering the type and extent of immune response. (I) and (II) have immunomodulatory, immunosuppressive and anti-allergic activities, and can be used in the modulation of immune responses via the stimulation of Th1 lymphocytes and Th1-associated cytokines, and suppression of Th2 lymphocytes and cytokines. The populations (I) and (II) of conjugate molecules may be used for modulating immune responses in individuals e.g. for the treatment of an allergic condition. (I) and (II) may be used to modulate immune responses and therefore prevent potentially harmful reactions to antigens. The present sequence represents an ISS polynucleotide which is used in the exemplification of the present invention.

CC Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTTGAGATGA 20

Db 15 GAACGTTGAGATGA 1

RESULT 69
AAFT7042/C
ID AAF77042 standard; DNA; 23 BP.

AAFT7042;

15-MAY-2001 (first entry)

Immunostimulatory DNA #2.

Modulate; immune; antigen; immunostimulatory; ds.

Synthetic.

WO200112223-A2.

22-FEB-2001.

18-AUG-2000; 2000WO-US22835.

19-AUG-1999; 99US-0149768.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Van Nest G;

WPI; 2001-211136/21.

Modulating immune response to a second antigen in humans involves administering an immunostimulatory polynucleotide comprising an immunostimulatory sequence and a first antigen

Disclosure; Page 15; 63pp; English.

The present invention relates to modulating an immune response to a second antigen in an individual, involving administering to the individual an immunostimulatory polynucleotide comprising an immunostimulatory sequence (ISS) and a first antigen.

Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 22; Length 23;

Best Local Similarity 100.0%; Pred. No. 19; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
15 GAACGTTGAGATGA 1

RESULT 70
AAS16339/C
ID AAS16339 standard; DNA; 23 BP.

AAS16339;

14-FEB-2002 (first entry)

ISS polynucleotide #3 useful for treating herpes virus infections.

Herpes simplex virus; HSV infection; immunostimulatory sequence; ISS; immune response; alphaherpesvirinae; herpes virus zoster virus; VZV; HSV-1; HSV-2; chicken pox; herpes labialis; cold sore; genital herpes; virucide; ss.

Synthetic.

WO200168103-A2.

XX

PD 20-SEP-2001.

12-MAR-2001; 2001WO-US07841.

10-MAR-2000; 2000US-18856P.

09-MAR-2001; 2001US-0802518.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

Van Nest G;

WPI; 2002-041171/05.

Preventing, reducing the severity or reducing the recurrence of an infection or symptom of herpes simplex virus (HSV), e.g. HSV-2, comprises administering an immunostimulatory sequence to an individual

Disclosure; Page 19; 49pp; English.

The present invention relates to novel methods of treating, preventing, or reducing the severity or recurrence of a symptom of herpes simplex virus (HSV) infection in an individual who has been exposed to or who is infected with HSV. The method comprises administering a polynucleotide having an immunostimulatory sequence (ISS; AAS16337-AAS16345) which induces an immune response. A composition containing ISS is administered without a HSV (alphaherpesvirinae) antigen. The composition of HSV infection caused by herpes virus zoster virus (VZV), HSV-1 and particularly HSV-2. Such HSV infections include chicken pox, herpes labialis (cold sores) and genital herpes. The present sequence represents one of the ISS polynucleotides of the invention.

Note: The present sequence is shown as single stranded in the specification, but the patentees state on page 20 that this sequence may be double stranded.

Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 24; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
15 GAACGTTGAGATGA 1

RESULT 71
AAS16350/C
ID AAS16350 standard; DNA; 23 BP.

AAS16350;

14-FEB-2002 (first entry)

ISS polynucleotide #3 useful for treating papillomavirus infections.

Animal papillomavirus infection; human papillomavirus; HPV; STD; wart; sexually transmitted disease; cervical cancer; immune response; immunostimulatory sequence; ISS; virucide; ss.

Synthetic.

WO200168117-A2.

20-SEP-2001.

12-MAR-2001; 2001WO-US07842.

10-MAR-2000; 2000US-188265P.

09-MAR-2001; 2001US-0802445.

(DYNA-) DYNAVAX TECHNOLOGIES CORP.

PA

XX	Van Nest G;
PI	
XX	WPI: 2002-041172/05.
DR	
XX	
PT	Treating, preventing or ameliorating papillomavirus infections,
PT	comprises administering a composition comprising a polynucleotide
PT	having an immunostimulatory sequence to the individual
XX	
PS	Disclosure; Page 20; 44pp; English.
XX	
CC	The present invention relates to novel methods of treating, preventing,
CC	or reducing the severity or recurrence of a symptom of papillomavirus
CC	infection in an individual that has been exposed to or who is infected
CC	with papillomavirus. The method comprises administering a polynucleotide
CC	having an immunostimulatory sequence (ISS; AAS16348-AAS16355) which
CC	induces an immune response. A composition containing ISS is administered
CC	without a papillomavirus antigen. The composition can be included in a
CC	kit for ameliorating or preventing a symptom of human or animal
CC	papillomavirus infection. Infections with human papillomavirus (HPV)
CC	which can be prevented or treated using the method of the invention
CC	include sexually transmitted diseases (STDs), warts, papillomas and
CC	cerical cancer. The present sequence represents one of the ISS
CC	polynucleotides of the invention.
CC	Note: The present sequence is shown as single stranded in the
CC	specification, but the patentees state on page 20 that this sequence may
CC	be double stranded.
XX	
SO	Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;
Query Match	71.4%; Score 15; DB 24; Length 23;
Best Local Similarity	100.0%; Pred. No. 19;
Matches 15; Conservative	0; Mismatches 0; Indels 0; Gaps 0.
Oy	6 GAACGTCGAGATGA 20
Db	15 GAACGTCGAGATGA 1
RESULT 72	
AAD21879	
ID	AAD21879 standard; DNA; 23 BP.
XX	
AC	AAD21879;
XX	
DT	12-FEB-2002 (first entry)
XX	
DE	Immunostimulatory sequence oligonucleotide (ISS-ODN) #2.
XX	
KW	Cytotoxic T lymphocyte; CTL; T cell; tumour load; cancer radiotherapy;
KW	immunostimulatory sequence oligonucleotide; ISS-ODN; chemotherapy;
KW	immunosuppression; transplantation; autoimmune disease; infection;
KW	acquired immune deficiency syndrome; AIDS; intracellular pathogen;
KW	cytomegalovirus; mycobacterial infection; Epstein-Barr virus;
KW	varicella zoster virus; human immunodeficiency virus; HIV;
KW	phosphorothioate backbone; ss.
XX	
OS	Unidentified.
XX	
FT	Key
FT	modified_base
FT	1..22
FT	Location/Qualifiers
FT	1..22
FT	/*tag= a
FT	/mod_base= OTHER
FT	/note= "Phosphorothioate backbone"
FT	23
FT	/*tag= b
FT	/note= "This residue is not found in the sequence
XX	shown in page 44 of the specification"
PN	WO200172123-A1.
XX	
PD	04-OCT-2001.
XX	

PF 28-MAR-2001; 2001WO-US10118.
PR 28-MAR-2000; 2000US-192537P.
PR 11-MAY-2000; 2000US-203567P.
PR 05-JUL-2000; 2000US-215895P.
XX
PA (REGC) UNIV CALIFORNIA.
PA (VERE-) DEPT VETERANS AFFAIRS.
XX
PI Raz E, Cho HJ, Richman DD, Horner AA;
XX
DR WPI; 2002-010699/01.
XX
PT Increasing antigen-specific cytotoxic T lymphocyte activity in a CD4+ T
PT cell deficient individual, useful to treat immunodeficiency and block
PT HIV infection, comprises administering immunostimulatory nucleic acid
PT
XX
PS Example 1; Page 53; 91pp; English.
XX
XX The present invention relates to a method for increasing antigen-specific
CC cytotoxic T lymphocyte (CTL) activity in a CD4+ T cell-deficient
CC individual, comprising administering an immunostimulatory sequence
CC oligonucleotide (ISS-ODN). The immunostimulatory nucleic acids of the
CC invention are used in CD4+ T cell-deficient individuals to decrease
CC tumor load, to treat a primary or acquired immunodeficiency,
CC particularly where the acquired immunodeficiency is temporary, and due
CC to cancer radiotherapy or chemotherapy or immunosuppression following
CC bone marrow or organ transplantation, or autoimmune disease treatment,
CC or is acquired immunodeficiency syndrome (AIDS). The nucleic acids may
CC be used to treat a person at risk of becoming CD4+ T cell-deficient,
CC particularly where someone at risk of cancer recurrence. They are also
CC used to treat infection, particularly by an intracellular pathogen,
CC especially one caused by cytomegalovirus, Mycobacterium tuberculosis,
CC M. avium, Epstein-Barr virus, a fungus yeast, varicella zoster virus or
CC human immunodeficiency virus (HIV). The present sequence is a
CC phosphorochioate immunostimulatory sequence oligonucleotide (ISS-ODN),
CC used in the exemplification of the invention.
XX
XX
SQ Sequence 23 BP; 6 A; 3 C; 7 G; 6 T; 1 other;
XX
Query Match 71.4%; Score 15; DB 24; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 GAACGTTGAGATGA 20
| | | | | | | | | |
Db 8 GAACGTTGAGATGA 22
RESULT 73
ID ABA03835/C
ID ABA03835 standard; DNA; 23 BP.
XX
AC ABA03835;
XX
DT 12-FEB-2002 (first entry)
XX
DE Immunostimulatory sequence (ISS) SEQ ID NO:3.
XX
XX Immunomodulatory polynucleotide/microcarrier complex; INF/MC; IgE;
XX immunomodulation; immunostimulation; phosphorochioate; immunomodulator;
XX antiallergic; antibacterial; antiprotocozal; antiparasitic; hepatotropic;
XX nephrotoxic; interferon-alpha stimulator; interferon-gamma stimulator;
XX immunoglobulin E stimulator; immune response; IPF; scleroderma; malaria;
XX idiopathic pulmonary fibrosis; cutaneous radiation-induced fibrosis;
XX hepatic fibrosis; renal fibrosis; infectious disease; leishmaniasis;
XX mycobacterial disease; toxoplasmosis; schistosomiasis; chlamorchiasis;
XX allergy; allergy-induced asthma; prophylactic vaccine; cancer; ss.
XX
OS Synthetic.
XX
PN WO200168144-A2.

[illegible]

PF	12-MAR-2001; 2001WO-US07840.
XX	
PR	10-MAR-2000; 2000US-188302P.
PR	09-MAR-2001; 2001US-0802685.
PA	(DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX	
PI	Van Nest G;
XX	
DR	WPI; 2002-048999/06.
XX	
PT	Reducing severity, recurrence or duration of symptom of virus
PT	infection, or reducing viremia or blood levels of virus antigen,
PT	comprises administering a polynucleotide having an immunostimulatory
PT	sequence -
XX	
PS	Disclosure; Page 20; 65pp; English.
XX	
CC	The present invention describes a method for reducing severity of a
CC	symptom of virus infection in an individual infected with a virus. The
CC	method comprises administering an individual consisting of a
CC	polynucleotide having an immunostimulatory sequence (ISS). The ISS
CC	comprises the sequence 5'-C,G,pyrimidine,pyrimidine,C,G-3'. An antigen
CC	is administered in conjunction with the composition. ISS has virulence
CC	activity and can be used in gene therapy. The method using the ISS can
CC	be used for suppressing, ameliorating and/or preventing viral infections
CC	to an individual who may be at risk of being exposed to, exposed to or
CC	infected by a virus. It may also be used in reducing the recurrence
CC	or duration of a symptom of viral infection, delaying the development
CC	of a virus infection, and reducing viremia or blood levels of virus
CC	antigens. The present sequence represents an ISS given in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;
XX	
Query Match	71.4%; Score 15; DB 24; Length 23;
Best Local Similarity	100.0%; Pred. No. 19;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	6 GAACGTCGAGATGA 20
DB	15 GAACGTCGAGATGA 1
XX	
RESULT 75	
ABA03858/C	
ID	ABA03858 standard; DNA; 23 BP.
XX	
AC	ABA03858;
XX	
DT	12-FEB-2002 (first entry)
XX	
DE	Immunostimulatory sequence (ISS) SEQ ID NO:3.
XX	
KM	Immunostimulatory sequence; ISS; immunomodulation; HBV; HCV; infection;
KM	hepatitis B virus; hepatitis C virus; virulence; anti-inflammatory;
KM	hepatotropic; gene therapy; hepatitis infection; viremia; jaundice;
KM	fatigue; abdominal pain; portal hypertension; cirrhosis; ss.
XX	
OS	Synthetic.
XX	
PN	WO200168078-A2.
XX	
PD	20-SEP-2001.
XX	
PF	12-MAR-2001; 2001WO-US07931.
XX	
PR	10-MAR-2000; 2000US-188301P.
PR	09-MAR-2001; 2001US-0802370.
XX	
PA	(DYNA-) DYNAVAX TECHNOLOGIES CORP.
XX	
PI	Van Nest G;

XX WPI; 2002-049000/06.

DR
XX
PT Reducing viremia and blood levels of hepatitis virus antigen in an
PT individual infected with hepatitis B virus, comprises administering a
PT composition comprising a polynucleotide having an immunostimulatory
PT sequence -

XX
PS Disclosure; Page 20; 43pp; English.

CC The present invention describes a method for reducing viraemia or blood
CC levels of a hepatitis virus antigen in an individual infected with
CC hepatitis B virus (HBV). The method comprises administering a composition
CC comprising a polynucleotide having an immunostimulatory sequence (ISS)
CC to the individual, where the ISS comprises the sequence 5'-C₁-G-3', an
CC HBV antigen is not administered in conjunction with administration of
CC the composition, and where the composition is administered in an amount
CC sufficient to reduce HBV viraemia or blood levels of a hepatitis virus
CC antigen. ISS has virucide, anti-inflammatory and hepatotropic activities,
CC and can be used in gene therapy. The method can be used for suppressing
CC and/or ameliorating hepatitis infection in an individual, especially for
CC preventing, palliating, ameliorating, reducing and/or eliminating one or
CC more symptoms of HBV or HCV (hepatitis C virus) infection without
CC administering HBV or HCV antigens. The method is specifically useful for
CC reducing viraemia and hepatitis viral antigen in blood. ISS-containing
CC polynucleotides may also be used to improve physical symptoms such as
CC jaundice, fatigue, abdominal pain, and other clinical/laboratory
CC findings associated with hepatitis such as blood levels of liver enzymes,
CC portal hypertension, or cirrhosis. The present sequence represents an
CC ISS oligonucleotide given in the exemplification of the present
CC invention.

XX
SQ Sequence 23 BP; 6 A; 8 C; 3 G; 6 T; 0 other;

Query Match 71.4%; Score 15; DB 24; Length 23;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTCGAGATGA 20
|||
Db 15 GAACGTCGAGATGA 1

Search completed: December 17, 2003, 09:18:02
Job time : 150 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2003, 09:38:49 : Search time 1152 Seconds
(without alignments)
60.743 Million cell updates/sec

Title: US-10-033-243-132

Perfect score: 21

Sequence: 1 tcgcgaacttcgagatgat 21

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 2211978 seqs, 1666101734 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4423956

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Published Applications NA:*

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10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	100.0	21	US-10-033-243-132	Sequence 132, App
2	19	90.5	19	US-09-927-422A-16	Sequence 16, Appl
3	19	90.5	19	US-10-176-883-41	Sequence 41, Appl
4	19	90.5	19	US-10-177-826-41	Sequence 41, Appl
5	19	90.5	19	US-10-033-243-19	Sequence 19, Appl
6	19	90.5	22	US-10-176-883-52	Sequence 52, Appl
7	19	90.5	22	US-10-177-826-52	Sequence 52, Appl
8	19	90.5	22	US-10-033-243-30	Sequence 30, Appl
9	16	76.2	18	US-10-176-883-36	Sequence 36, Appl
10	16	76.2	18	US-10-177-826-36	Sequence 36, Appl
11	16	76.2	18	US-10-033-243-14	Sequence 14, Appl
12	16	76.2	66	US-10-176-883-139	Sequence 139, App
13	16	76.2	66	US-10-177-826-139	Sequence 139, App
14	15	71.4	20	US-09-848-986-21	Sequence 21, Appl
15	15	71.4	20	US-10-233-121A-21	Sequence 21, Appl

16	15	71.4	22	9	US-09-802-666-1	Sequence 1, Appl
17	15	71.4	22	9	US-09-802-666-2	Sequence 2, Appl
18	15	71.4	22	9	US-09-802-665-1	Sequence 1, Appl
19	15	71.4	22	9	US-09-802-665-2	Sequence 2, Appl
20	15	71.4	22	9	US-09-791-500-1	Sequence 1, Appl
21	15	71.4	22	9	US-09-802-376-1	Sequence 1, Appl
22	15	71.4	22	9	US-09-802-376-2	Sequence 2, Appl
23	15	71.4	22	9	US-09-802-370-1	Sequence 1, Appl
24	15	71.4	22	9	US-09-802-370-2	Sequence 2, Appl
25	15	71.4	22	10	US-09-802-445-1	Sequence 1, Appl
26	15	71.4	22	10	US-09-802-445-2	Sequence 2, Appl
27	15	71.4	22	10	US-09-820-484-1	Sequence 1, Appl
28	15	71.4	22	10	US-09-820-484-3	Sequence 3, Appl
29	15	71.4	22	10	US-09-828-505-1	Sequence 1, Appl
30	15	71.4	22	10	US-09-967-881-2	Sequence 2, Appl
31	15	71.4	22	11	US-09-927-422A-1	Sequence 1, Appl
32	15	71.4	22	11	US-09-927-422A-2	Sequence 2, Appl
33	15	71.4	22	11	US-09-738-046A-3	Sequence 3, Appl
34	15	71.4	22	11	US-09-927-884-1	Sequence 1, Appl
35	15	71.4	22	11	US-09-927-884-2	Sequence 2, Appl
36	15	71.4	22	13	US-09-802-359-1	Sequence 1, Appl
37	15	71.4	22	13	US-09-802-359-2	Sequence 2, Appl
38	15	71.4	22	13	US-09-967-864-19	Sequence 19, Appl
39	15	71.4	22	13	US-10-214-799-2	Sequence 2, Appl
40	15	71.4	22	13	US-10-340-275-1	Sequence 1, Appl
41	15	71.4	22	13	US-10-340-275-3	Sequence 3, Appl
42	15	71.4	22	13	US-10-339-885-1	Sequence 1, Appl
43	15	71.4	22	13	US-10-339-885-3	Sequence 3, Appl
44	15	71.4	22	13	US-09-848-986-1	Sequence 1, Appl
45	15	71.4	22	13	US-10-176-883-2	Sequence 2, Appl
46	15	71.4	22	13	US-10-176-883-4	Sequence 4, Appl
47	15	71.4	22	13	US-10-176-883-14	Sequence 14, Appl
48	15	71.4	22	13	US-10-176-883-79	Sequence 79, Appl
49	15	71.4	22	13	US-10-176-883-84	Sequence 84, Appl
50	15	71.4	22	13	US-10-176-883-85	Sequence 85, Appl
51	15	71.4	22	13	US-10-176-883-134	Sequence 134, App
52	15	71.4	22	13	US-10-176-883-140	Sequence 140, App
53	15	71.4	22	13	US-10-176-883-141	Sequence 141, App
54	15	71.4	22	13	US-10-412-151-1	Sequence 1, Appl
55	15	71.4	22	13	US-10-177-826-2	Sequence 2, Appl
56	15	71.4	22	13	US-10-177-826-24	Sequence 24, Appl
57	15	71.4	22	13	US-10-177-826-44	Sequence 44, Appl
58	15	71.4	22	13	US-10-177-826-79	Sequence 79, Appl
59	15	71.4	22	13	US-10-177-826-85	Sequence 85, Appl
60	15	71.4	22	13	US-10-177-826-85	Sequence 85, Appl
61	15	71.4	22	13	US-10-177-826-85	Sequence 85, Appl
62	15	71.4	22	13	US-10-177-826-85	Sequence 85, Appl
63	15	71.4	22	13	US-10-177-826-134	Sequence 134, App
64	15	71.4	22	13	US-10-177-826-140	Sequence 140, App
65	15	71.4	22	13	US-10-177-826-141	Sequence 141, App
66	15	71.4	22	13	US-10-357-760-1	Sequence 1, Appl
67	15	71.4	22	13	US-10-357-760-2	Sequence 2, Appl
68	15	71.4	22	15	US-10-056-420-4	Sequence 4, Appl
69	15	71.4	22	15	US-10-033-243-2	Sequence 2, Appl
70	15	71.4	22	15	US-10-033-243-12	Sequence 12, Appl
71	15	71.4	22	15	US-10-033-243-40	Sequence 40, Appl
72	15	71.4	22	15	US-10-033-243-45	Sequence 45, Appl
73	15	71.4	22	15	US-10-033-243-46	Sequence 46, Appl
74	15	71.4	22	15	US-10-033-243-59	Sequence 59, Appl
75	15	71.4	22	15	US-10-033-243-59	Sequence 59, Appl
76	15	71.4	22	15	US-10-033-243-59	Sequence 59, Appl
77	15	71.4	22	15	US-10-229-088-19	Sequence 19, Appl
78	15	71.4	22	15	US-10-229-088-19	Sequence 19, Appl
79	15	71.4	22	15	US-10-229-088-19	Sequence 19, Appl
80	15	71.4	22	16	US-10-219-143-1	Sequence 1, Appl
81	15	71.4	22	16	US-09-802-666-3	Sequence 3, Appl
82	15	71.4	23	9	US-09-802-665-3	Sequence 3, Appl
83	15	71.4	23	9	US-09-802-376-3	Sequence 3, Appl
84	15	71.4	23	9	US-09-802-370-3	Sequence 3, Appl
85	15	71.4	23	10	US-09-802-445-3	Sequence 3, Appl
86	15	71.4	23	11	US-09-927-422A-3	Sequence 3, Appl
87	15	71.4	23	11	US-09-927-884-3	Sequence 3, Appl
88	15	71.4	23	13	US-09-802-359-3	Sequence 3, Appl

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c 89 15 71.4 23 13 US-10-357-760-3 Sequence 3, Appli
90 14 66.7 14 13 US-10-176-883-98 Sequence 98, Appl
91 14 66.7 14 13 US-10-176-883-104 Sequence 104, Appl
92 14 66.7 14 13 US-10-177-826-98 Sequence 98, Appl
93 14 66.7 14 13 US-10-177-826-104 Sequence 104, Appl
94 14 66.7 14 13 US-10-033-243-98 Sequence 98, Appl
95 14 66.7 16 13 US-10-176-883-33 Sequence 33, Appl
96 14 66.7 16 13 US-10-177-826-33 Sequence 33, Appl
97 14 66.7 16 15 US-10-033-243-11 Sequence 11, Appl
98 14 66.7 18 13 US-10-176-883-51 Sequence 51, Appl
99 14 66.7 18 13 US-10-176-883-83 Sequence 83, Appl
100 14 66.7 18 13 US-10-177-826-51 Sequence 51, Appl
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ALIGNMENTS

```
RESULT 1
US-10-033-243-132
; Sequence 132, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: PEARON, Karen L.
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; FILE REFERENCE: 37782001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 132
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-132
```

```
Query Match 100.0%; Score 21; DB 15; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGTGAACGTTGAGATGAT 21
DB 1 TCGTGAACGTTGAGATGAT 21
```

```
RESULT 2
US-09-927-422A-16
; Sequence 16, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Fearon, Stephen
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
; FILE REFERENCE: 37782001420
; CURRENT APPLICATION NUMBER: US/09/927,422A
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 16
; LENGTH: 19
; TYPE: DNA
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-16
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Query Match 90.5%; Score 19; DB 11; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 TCGTGAACGTTGAGATG 19
DB 1 TCGTGAACGTTGAGATG 19
```

```
RESULT 3
US-10-176-883-41
; Sequence 41, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 37782002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 41
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-176-883-41
```

```
Query Match 90.5%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 TCGTGAACGTTGAGATG 19
DB 1 TCGTGAACGTTGAGATG 19
```

```
RESULT 4
US-10-177-826-41
; Sequence 41, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 37782002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 41
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
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FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-177-826-41

Query Match 90.5%; Score 19; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTCCGAGATG 19
|||||
DB 1 TCGTCGAACGTTCCGAGATG 19

RESULT 5
US-10-033-243-19
Sequence 19, Application US/10033243
Publication No. US20030049266A1
GENERAL INFORMATION:
APPLICANT: FEARON, Karen L.
APPLICANT: DINA, Dino
TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
FILE REFERENCE: 37782001800
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 60/375,253
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 133
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleotide containing CG

US-10-033-243-19

Query Match 90.5%; Score 19; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTCCGAGATG 19
|||||
DB 1 TCGTCGAACGTTCCGAGATG 19

RESULT 6
US-10-176-883-52
Sequence 52, Application US/10176883
Publication No. US20030175731A1
GENERAL INFORMATION:
APPLICANT: FEARON, Karen
APPLICANT: DINA, Dino
APPLICANT: TUCK, Stephen
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
FILE REFERENCE: 37782002000
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/299,883
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/375,253
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-176-883-52

Query Match 90.5%; Score 19; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 90.5%; Score 19; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTCCGAGATG 19
|||||
DB 4 TCGTCGAACGTTCCGAGATG 22

RESULT 7
US-10-177-826-52
Sequence 52, Application US/10177826
Publication No. US20030199466A1
GENERAL INFORMATION:
APPLICANT: FEARON, Karen
APPLICANT: DINA, Dino
APPLICANT: TUCK, Stephen
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
FILE REFERENCE: 37782002001
CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/299,883
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/375,253
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 52
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-177-826-52

Query Match 90.5%; Score 19; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGAACGTTCCGAGATG 19
|||||
DB 4 TCGTCGAACGTTCCGAGATG 22

RESULT 8
US-10-033-243-30
Sequence 30, Application US/10033243
Publication No. US20030049266A1
GENERAL INFORMATION:
APPLICANT: FEARON, Karen L.
APPLICANT: DINA, Dino
TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
FILE REFERENCE: 37782001800
CURRENT FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: 60/258,675
PRIOR FILING DATE: 2000-12-27
NUMBER OF SEQ ID NOS: 133
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-30

Query Match 90.5%; Score 19; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTGAACGTTGCAGATG 19
|||
Db 4 TCGTGAACGTTGCAGATG 22

RESULT 9
US-10-176-883-36

; Sequence 36, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-176-883-36

Query Match 76.2%; Score 16; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TCGAACGTTGCAGATG 19
|||
Db 3 TCGAACGTTGCAGATG 18

RESULT 10
US-10-177-826-36

; Sequence 36, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-36

Query Match 76.2%; Score 16; DB 13; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TCGAACGTTGCAGATG 19

Db 3 TCGAACGTTGCAGATG 18
|||
|||

RESULT 11
US-10-033-243-14

; Sequence 14, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
; TITLE OF INVENTION: METHODS OF USING THE SAME
; FILE REFERENCE: 377882001800
; CURRENT APPLICATION NUMBER: US/10/033,243
; CURRENT FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: 60/258,675
; PRIOR FILING DATE: 2000-12-27
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-14

Query Match 76.2%; Score 16; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 TCGAACGTTGCAGATG 19
|||
Db 3 TCGAACGTTGCAGATG 18

RESULT 12
US-10-176-883-139

; Sequence 139, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-176-883-139

Query Match 76.2%; Score 16; DB 13; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GAACGTTGCAGATGAT 21
|||
Db 8 GAACGTTGCAGATGAT 23

RESULT 13
US-10-177-826-139
; Sequence 139, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-11
; FILE REFERENCE: 37782002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 66
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-139

Query Match 76.2%; Score 16; DB 13; Length 66;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 21
|||
DB 8 GAACGTTGAGATGA 23

RESULT 14
US-09-848-986-21
; Sequence 21, Application US/09848986
; Publication No. US20030176373A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Loie, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; TITLE OF INVENTION: Methods of Use Thereof
; FILE REFERENCE: 06510168US1
; CURRENT APPLICATION NUMBER: US/09/848,986
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: us 60/262321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: us 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ISS-ODN
US-09-848-986-21

Query Match 71.4%; Score 15; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||
DB 6 GAACGTTGAGATGA 20

RESULT 15

US-10-233-121A-21
; Sequence 21, Application US/10233121A
; Publication No. US20030125284A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, EYAL
; APPLICANT: LOIS, AUGUSTO
; APPLICANT: TAKABAYASHI, KENJI
; TITLE OF INVENTION: AGENTS THAT MODULATE DNA-PK ACTIVITY AND
; TITLE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: UCAL-168DIV
; CURRENT APPLICATION NUMBER: US/10/233,121A
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/848,986
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: us 60/202,274
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/262,321
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphodiester or phosphorothioate oligonucleotide
US-10-233-121A-21

Query Match 71.4%; Score 15; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||
DB 6 GAACGTTGAGATGA 20

RESULT 16
US-09-802-686-1
; Sequence 1, Application US/09802686
; Patent No. US20010046967A1
; GENERAL INFORMATION:
; APPLICANT: Dynavax Technologies Corporation
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
; TITLE OF INVENTION: RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
; FILE REFERENCE: 37782000900
; CURRENT APPLICATION NUMBER: US/09/802,686
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,583
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-686-1

Query Match 71.4%; Score 15; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||
DB 8 GAACGTTGAGATGA 22

RESULT 17
US-09-802-686-2

```
; Sequence 2, Application US/09802686
; Patent No. US20010046967A1
; GENERAL INFORMATION:
; APPLICANT: Dynavax Technologies Corporation
; APPLICANT: Van Nest, Gary
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING
; TITLE OF INVENTION: RESPIRATORY VIRAL INFECTION USING IMMUNOMODULATORY
; FILE REFERENCE: 37782000900
; CURRENT APPLICATION NUMBER: US/09/802,686
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,583
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-686-2

Query Match      71.4%; Score 15; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 18
US-09-802-685-1
; Sequence 1, Application US/09802685
; Patent No. US20020028784A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Eiden, Joseph J., Jr.
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING VIRAL
; TITLE OF INVENTION: INFECTIONS USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882001600
; CURRENT APPLICATION NUMBER: US/09/802,685
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,302
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-685-1

Query Match      71.4%; Score 15; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 19
US-09-802-685-2
; Sequence 2, Application US/09802685
; Patent No. US20020028784A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Eiden, Joseph J., Jr.
; TITLE OF INVENTION: METHODS OF PREVENTING AND TREATING VIRAL
```

```
; TITLE OF INVENTION: INFECTIONS USING IMMUNOMODULATORY POLYNUCLEOTIDE SEQUENCES
; FILE REFERENCE: 377882001600
; CURRENT APPLICATION NUMBER: US/09/802,685
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,302
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-685-2

Query Match      71.4%; Score 15; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 20
US-09-791-500-1
; Sequence 1, Application US/09791500
; Patent No. US20020042387A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; TITLE OF INVENTION: Disease and Other Forms of Gastrointestinal Inflammation.
; FILE REFERENCE: 6510-202US1
; CURRENT APPLICATION NUMBER: US/09/791,500
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
US-09-791-500-1

Query Match      71.4%; Score 15; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 21
US-09-802-376-1
; Sequence 1, Application US/09802376
; Patent No. US20020055477A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 37788201700
; CURRENT APPLICATION NUMBER: US/09/802,376
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
```

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-1

Query Match 71.4%; Score 15; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||||
DB 8 GAACGTTGAGATGA 22

RESULT 22
US-09-802-376-2
Sequence 2, Application US/09802376
Patent No. US2002005477A1
GENERAL INFORMATION:
APPLICANT: Van Nest, Gary
APPLICANT: Tuck, Stephen
TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
FILE REFERENCE: 37788201700
CURRENT APPLICATION NUMBER: US/09/802,376
CURRENT FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 60/188,557
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleotide containing CG
US-09-802-376-2

Query Match 71.4%; Score 15; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||||
DB 8 GAACGTTGAGATGA 22

RESULT 23
US-09-802-370-1
Sequence 1, Application US/09802370
Patent No. US20020098199A1
GENERAL INFORMATION:
APPLICANT: Van Nest, Gary
APPLICANT: Eiden, Joseph J. Jr.
TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
FILE REFERENCE: 377882001200
CURRENT APPLICATION NUMBER: US/09/802,370
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/188,301
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleotide containing CG
US-09-802-370-1

Query Match 71.4%; Score 15; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 GAACGTTGAGATGA 20
|||||
DB 8 GAACGTTGAGATGA 22

RESULT 24
US-09-802-370-2
Sequence 2, Application US/09802370
Patent No. US20020098199A1
GENERAL INFORMATION:
APPLICANT: Van Nest, Gary
APPLICANT: Eiden, Joseph J. Jr.
TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
FILE REFERENCE: 377882001200
CURRENT APPLICATION NUMBER: US/09/802,370
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/188,301
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleotide containing CG
US-09-802-370-2

Query Match 71.4%; Score 15; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||||
DB 8 GAACGTTGAGATGA 22

RESULT 25
US-09-802-445-1
Sequence 1, Application US/09802445
Patent No. US20020107212A1
GENERAL INFORMATION:
APPLICANT: Van Nest, Gary
APPLICANT: Eiden, Joseph J. Jr.
TITLE OF INVENTION: METHODS OF REDUCING PAPILLOMAVIRUS INFECTION USING IMMUNOMODULATO
FILE REFERENCE: 377882001300
CURRENT APPLICATION NUMBER: US/09/802,445
CURRENT FILING DATE: 2001-09-24
PRIOR APPLICATION NUMBER: 60/188,265
PRIOR FILING DATE: 2000-03-10
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 22
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Polynucleotide containing CG
US-09-802-445-1

Query Match 71.4%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||||
DB 8 GAACGTTGAGATGA 22

RESULT 26
US-09-802-445-2
; Sequence 2, Application US/09802445
; Patent No. US20020107212A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Elden, Joseph J. Jr.
; TITLE OF INVENTION: METHODS OF REDUCING PAPILLOMAVIRUS INFECTION USING IMMUNOMODULATOR
; FILE REFERENCE: 377882001300
; CURRENT APPLICATION NUMBER: US/09/802,445
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/188,265
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-445-2

Query Match 71.4%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||||
DB 8 GAACGTTGAGATGA 22

RESULT 27
US-09-820-484-1
; Sequence 1, Application US/09820484
; Patent No. US20020142977A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188US1
; CURRENT APPLICATION NUMBER: US/09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
; NAME/KEY: modified base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
US-09-820-484-1

Query Match 71.4%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||||
DB 8 GAACGTTGAGATGA 22

RESULT 28
US-09-820-484-3
; Sequence 3, Application US/09820484
; Patent No. US20020142977A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188US1
; CURRENT APPLICATION NUMBER: US/09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorothioate ISS-ODN
US-09-820-484-3

Query Match 71.4%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||||
DB 8 GAACGTTGAGATGA 22

RESULT 29
US-09-828-505-1
; Sequence 1, Application US/09828505
; Patent No. US20020142978A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Takabayashi, Kenji
; APPLICANT: Nguyen, Minh-Duc
; TITLE OF INVENTION: Synergistic Improvements to
; TITLE OF INVENTION: Polynucleotide Vaccines
; FILE REFERENCE: 6510-203
; CURRENT APPLICATION NUMBER: US/09/828,505
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,890
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory nucleic acid sequence
US-09-828-505-1

Query Match 71.4%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||||
DB 8 GAACGTTGAGATGA 22


```
RESULT 30
US-09-967-881-2
; Sequence 2, Application US/09967881
; Publication No. US20020192184A1
; GENERAL INFORMATION:
; APPLICANT: Assistance Publique - Hopitaux de Paris
; APPLICANT: Institut National de la Sante et de la Recherche M
; APPLICANT: Carpentier, Antoine
; TITLE OF INVENTION: Use of Stabilised Oligonucleotides for Preparing A Medicament wit
; TITLE OF INVENTION: Antitumor Activity
; FILE REFERENCE: 267/246 US
; CURRENT APPLICATION NUMBER: US/09/967,881
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligodeoxynucleotide
US-09-967-881-2

Query Match          71.4%; Score 15; DB 10; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 31
US-09-927-422A-1
; Sequence 1, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
; TITLE OF INVENTION: FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 377882001420
; CURRENT APPLICATION NUMBER: US/09/927,422A
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,30
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-1

Query Match          71.4%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 32
US-09-927-422A-2
```

```
; Sequence 2, Application US/09927422A
; Publication No. US20030022852A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: BIODEGRADABLE IMMUNOMODULATORY
; TITLE OF INVENTION: FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 377882001420
; CURRENT APPLICATION NUMBER: US/09/927,422A
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/802,359
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,30
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-927-422A-2

Query Match          71.4%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 33
US-09-738-046A-3
; Sequence 3, Application US/09738046A
; Publication No. US20030054007A1
; GENERAL INFORMATION:
; APPLICANT: FELGNER, PHILIP L.
; APPLICANT: ZELPHART, OLIVIER
; TITLE OF INVENTION: INTRACELLULAR PROTEIN DELIVERY
; TITLE OF INVENTION: COMPOSITIONS AND METHODS OF USE
; FILE REFERENCE: GTSYS.004A
; CURRENT APPLICATION NUMBER: US/09/738,046A
; CURRENT FILING DATE: 2000-12-15
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence containing Cpg sequence
US-09-738-046A-3

Query Match          71.4%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
DB      8 GAACGTTGAGATGA 22

RESULT 34
US-09-927-884-1
; Sequence 1, Application US/09927884
; Publication No. US20030059773A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
```

```

; APPLICANT: Fearon, Karen L.
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND
; FILE REFERENCE: 37782001720
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US/09/927,884
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,557
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-927-884-1

```

```

Query Match          71.4%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

```

```

RESULT 35
US-09-927-884-2
; Sequence 2, Application US/09927884
; Publication No. US20030059773A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; APPLICANT: Fearon, Karen L.
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND
; FILE REFERENCE: 37782001720
; CURRENT APPLICATION NUMBER: US/09/927,884
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: U.S. 09/802,376
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: U.S. 60/188,557
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-927-884-2

```

```

Query Match          71.4%; Score 15; DB 11; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

```

```

RESULT 36
US-09-802-359-1
; Sequence 1, Application US/09802359
; Publication No. US20030129251A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary

```

```

; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 3778201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-1

```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

```

```

RESULT 37
US-09-802-359-2
; Sequence 2, Application US/09802359
; Publication No. US20030129251A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: IMMUNOMODULATORY FORMULATIONS AND METHODS FOR USE THEREOF
; FILE REFERENCE: 3778201400
; CURRENT APPLICATION NUMBER: US/09/802,359
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,303
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-09-802-359-2

```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

```

```

RESULT 38
US-09-967-464-19
; Sequence 19, Application US/09967464
; Publication No. US20030138453A1
; GENERAL INFORMATION:
; APPLICANT: O'Hagan, Derek
; APPLICANT: Otten, Gillis
; APPLICANT: Donnelly, John J.
; APPLICANT: Polo, John M.
; APPLICANT: Barnett, Susan
; APPLICANT: Singh, Mamohan
; APPLICANT: Ulmer, Jeffrey
; APPLICANT: Dubensky, Jr., Thomas W.
; TITLE OF INVENTION: MICROPARTICLES FOR DELIVERY OF HETEROLOGOUS NUCLEIC ACIDS
; FILE REFERENCE: PPI6269.004

```

```

; CURRENT APPLICATION NUMBER: US/09/967,464
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/236,105
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: 60/315,905
; PRIOR FILING DATE: 2001-08-30
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial sequence is synthesized
US-09-967-464-19

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
        |||||||
DB      8 GAACGTCGAGATGA 22

RESULT 39
US-10-214-799-2
; Sequence 2, Application US/10214799
; Publication No. US20030133988A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen L. and Dina, Dino
; TITLE OF INVENTION: IMMUNOMODULATORY COMPOSITIONS,
; FILE REFERENCE: 37782003100
; CURRENT APPLICATION NUMBER: US/10/214,799
; CURRENT FILING DATE: 2002-08-07
; PRIOR APPLICATION NUMBER: US 60/310,743
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US 60/335,263
; PRIOR FILING DATE: 2001-10-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-214-799-2

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
        |||||||
DB      8 GAACGTCGAGATGA 22

RESULT 40
US-10-340-275-1
; Sequence 1, Application US/10340275
; Publication No. US20030143213A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; FILE REFERENCE: UCAL-188DIV
; CURRENT APPLICATION NUMBER: US/10/340,275
; CURRENT FILING DATE: 2003-01-10
```

```

; PRIOR APPLICATION NUMBER: 09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
US-10-340-275-1

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
        |||||||
DB      8 GAACGTCGAGATGA 22

RESULT 41
US-10-340-275-3
; Sequence 3, Application US/10340275
; Publication No. US20030143213A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; FILE REFERENCE: UCAL-188DIV
; CURRENT APPLICATION NUMBER: US/10/340,275
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorothioate ISS-ODN
US-10-340-275-3

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
        |||||||
DB      8 GAACGTCGAGATGA 22

RESULT 42
```

```
US-10-339-885-1
; Sequence 1, Application US/10339885
; Publication No. US20030147870A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Anthony A.
; APPLICANT: Horner, Douglas
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; FILE REFERENCE: UCAL-188CON
; CURRENT APPLICATION NUMBER: US/10/339,885
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
US-10-339-885-1
Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 43
US-10-339-885-3
; Sequence 3, Application US/10339885
; Publication No. US20030147870A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; FILE REFERENCE: UCAL-188CON
; CURRENT APPLICATION NUMBER: US/10/339,885
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 09/820,484
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: phosphorothioate ISS-ODN
US-10-339-885-3
Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 44
US-09-848-986-1
; Sequence 1, Application US/09848986
; Publication No. US20030176373A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Lois, Augusto F.
; APPLICANT: Takabayashi, Kenji
; TITLE OF INVENTION: Agents that Modulate DNA-PK Activity and
; FILE REFERENCE: 06510168US1
; CURRENT APPLICATION NUMBER: US/09/848,986
; CURRENT FILING DATE: 2001-05-03
; PRIOR APPLICATION NUMBER: us 60/262321
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: us 60/202,274
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: ISS-ODN
US-09-848-986-1
Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
Db      8 GAACGTCGAGATGA 22

RESULT 45
US-10-176-883-2
; Sequence 2, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
```

US-10-176-883-2

Query Match 71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22

RESULT 46

US-10-176-883-24
; Sequence 24, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:

APPLICANT: Fearon, Karen
APPLICANT: Dina, Dino
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
TITLE OF INVENTION: METHODS OF USING THE SAME-I
FILE REFERENCE: 377882002000

CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/299,883
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/375,253
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 22

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-176-883-24

Query Match 71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22

RESULT 47

US-10-176-883-34
; Sequence 34, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:

APPLICANT: Fearon, Karen
APPLICANT: Dina, Dino
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
TITLE OF INVENTION: METHODS OF USING THE SAME-I
FILE REFERENCE: 377882002000

CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/299,883
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/375,253
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 34
LENGTH: 22

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-176-883-34

Query Match 71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GAACGTCGAGATGA 20
|||||
Db 8 GAACGTCGAGATGA 22

RESULT 48

US-10-176-883-44
; Sequence 44, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:

APPLICANT: Fearon, Karen
APPLICANT: Dina, Dino
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
TITLE OF INVENTION: METHODS OF USING THE SAME-I
FILE REFERENCE: 377882002000

CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/299,883
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/375,253
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 22

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-176-883-44

Query Match 71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCGTCGAACGTTTGA 15
|||||
Db 1 TCGTCGAACGTTTGA 15

RESULT 49

US-10-176-883-79
; Sequence 79, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:

APPLICANT: Fearon, Karen
APPLICANT: Dina, Dino
TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
TITLE OF INVENTION: METHODS OF USING THE SAME-I
FILE REFERENCE: 377882002000

CURRENT FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: 60/299,883
PRIOR FILING DATE: 2001-06-21
PRIOR APPLICATION NUMBER: 60/375,253
PRIOR FILING DATE: 2002-04-23
NUMBER OF SEQ ID NOS: 141
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 79
LENGTH: 22

TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic construct
US-10-176-883-79

```
Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
        |||||
        8 GAACGTTGAGATGA 22

RESULT 50
US-10-176-883-84
; Sequence 84, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: variation
; LOCATION: 2, 5
; OTHER INFORMATION: n = 5-bromocytosine
US-10-176-883-84

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
        |||||
        8 GAACGTTGAGATGA 22

RESULT 51
US-10-176-883-85
; Sequence 85, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: Synthetic construct
; FEATURE:
; NAME/KEY: variation
; LOCATION: 5
; OTHER INFORMATION: n = 5-bromocytosine
US-10-176-883-85

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
        |||||
        8 GAACGTTGAGATGA 22

RESULT 52
US-10-176-883-134
; Sequence 134, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-176-883-134

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGATGA 20
        |||||
        8 GAACGTTGAGATGA 22

RESULT 53
US-10-176-883-140
; Sequence 140, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-I
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 22
```

```

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: n = thymine attached to a reactive linking group
US-10-176-883-140
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTTGAGATGA 20
        |||
        8 GAACGTTGAGATGA 22
```

RESULT 54

```

US-10-176-883-141
; Sequence 141, Application US/10176883
; Publication No. US20030175731A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002000
; CURRENT APPLICATION NUMBER: US/10/176,883
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: n = thymine attached to a reactive linking group
US-10-176-883-141
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTTGAGATGA 20
        |||
        8 GAACGTTGAGATGA 22
```

RESULT 55

```

US-10-412-151-1
; Sequence 1, Application US/10412151
; Publication No. US20030176389A1
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Rachmilewitz, Daniel
; TITLE OF INVENTION: Method for Treating Inflammatory Bowel
; FILE REFERENCE: UCAL-202CON
; CURRENT APPLICATION NUMBER: US/10/412,151
; PRIOR FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: 09/791,500
; PRIOR FILING DATE: 2001-02-22
```

```

; PRIOR APPLICATION NUMBER: 60/184,256
; PRIOR FILING DATE: 2000-02-23
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic polynucleotide sequence
; OTHER INFORMATION: oligonucleotide primer
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-10-412-151-1
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTTGAGATGA 20
        |||
        8 GAACGTTGAGATGA 22
```

RESULT 56

```

US-10-177-826-2
; Sequence 2, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-2
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      6 GAACGTTGAGATGA 20
        |||
        8 GAACGTTGAGATGA 22
```

RESULT 57

```

US-10-177-826-24
; Sequence 24, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; PRIOR FILING DATE: 2002-06-21
```

```

; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-24

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
      |||||:|||||
Db      8 GAACGTCGAGATGA 22
```

```

RESULT 58
US-10-177-826-34
; Sequence 34, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-34
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
      |||||:|||||
Db      8 GAACGTCGAGATGA 22
```

```

RESULT 59
US-10-177-826-44
; Sequence 44, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
```

```

; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-44

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGTCGAACGTTGCA 15
      |||||:|||||
Db      1 TCGTCGAACGTTGCA 15
```

```

RESULT 60
US-10-177-826-79
; Sequence 79, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-79
```

```

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
      |||||:|||||
Db      8 GAACGTCGAGATGA 22
```

```

RESULT 61
US-10-177-826-84
; Sequence 84, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
```



```
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 84
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: variation
; LOCATION: 2, 5
; OTHER INFORMATION: n = 5-bromocytosine
US-10-177-826-84

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

RESULT 62
US-10-177-826-85
; Sequence 85, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 85
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: variation
; LOCATION: 5
; OTHER INFORMATION: n = 5-bromocytosine
US-10-177-826-85

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

RESULT 63
US-10-177-826-134
; Sequence 134, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
```

```
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-177-826-134

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

RESULT 64
US-10-177-826-140
; Sequence 140, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
; APPLICANT: Fearon, Karen
; APPLICANT: Dina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; TITLE OF INVENTION: METHODS OF USING THE SAME-II
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 140
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: n = thymine attached to a reactive linking group
US-10-177-826-140

Query Match          71.4%; Score 15; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GAACGTCGAGATGA 20
        |||||||
Db      8 GAACGTCGAGATGA 22

RESULT 65
US-10-177-826-141
; Sequence 141, Application US/10177826
; Publication No. US20030199466A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Fearon, Karen
; APPLICANT: Tina, Dino
; APPLICANT: Tuck, Stephen
; TITLE OF INVENTION: CHIMERIC IMMUNOMODULATORY COMPOUNDS AND
; FILE REFERENCE: 377882002001
; CURRENT APPLICATION NUMBER: US/10/177,826
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: 60/299,883
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/375,253
; PRIOR FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 141
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
; NAME/KEY: modified_base
; LOCATION: 1
; OTHER INFORMATION: n = thymine attached to a reactive linking group
US-10-177-826-141
```

Query Match 71.4%; Score 15; DB 13; Length 22;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 6 GAACGTTGCAGATGA 20
Db 8 GAACGTTGCAGATGA 22
```

```
RESULT 66
US-10-357-760-1
; Sequence 1, Application US/10357760
; Publication No. US20030216340A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Eiden, Joseph J. Jr.
; TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
; FILE REFERENCE: 377882001200
; CURRENT APPLICATION NUMBER: US/10/357,760
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/802,370
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/188,301
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-357-760-1
```

Query Match 71.4%; Score 15; DB 13; Length 22;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 6 GAACGTTGCAGATGA 20
Db 8 GAACGTTGCAGATGA 22
```

```
RESULT 67
US-10-357-760-2
; Sequence 2, Application US/10357760
```

```
; Publication No. US20030216340A1
; GENERAL INFORMATION:
; APPLICANT: Van Nest, Gary
; APPLICANT: Eiden, Joseph J. Jr.
; TITLE OF INVENTION: METHODS OF SUPPRESSING HEPATITIS VIRUS
; FILE REFERENCE: 377882001200
; CURRENT APPLICATION NUMBER: US/10/357,760
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: US/09/802,370
; PRIOR FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/188,301
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polynucleotide containing CG
US-10-357-760-2
```

Query Match 71.4%; Score 15; DB 13; Length 22;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 6 GAACGTTGCAGATGA 20
Db 8 GAACGTTGCAGATGA 22
```

```
RESULT 68
US-10-056-420-4
; Sequence 4, Application US/10056420
; Publication No. US2003004428A1
; GENERAL INFORMATION:
; APPLICANT: Moss, Ronald B.
; APPLICANT: Carlo, Dennis J.
; TITLE OF INVENTION: Method For Treating an HIV-Infected
; TITLE OF INVENTION: Individual By Combining Immunization With Structured
; FILE REFERENCE: P-1M 5158
; CURRENT APPLICATION NUMBER: US/10/056,420
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: US 60/264,476
; PRIOR FILING DATE: 2001-01-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: exemplary ISS sequence
US-10-056-420-4
```

Query Match 71.4%; Score 15; DB 15; Length 22;

Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 6 GAACGTTGCAGATGA 20
Db 8 GAACGTTGCAGATGA 22
```

```
RESULT 69
US-10-033-243-2
; Sequence 2, Application US/10033243
; Publication No. US20030049266A1
; GENERAL INFORMATION:
; APPLICANT: FEARON, Karen L.
; APPLICANT: DINA, Dino
```

```
/ TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
/ FILE OF INVENTION: METHODS OF USING THE SAME
/ FILE REFERENCE: 37782001800
/ CURRENT APPLICATION NUMBER: US/10/033,243
/ CURRENT FILING DATE: 2002-04-03
/ PRIOR APPLICATION NUMBER: 60/258,675
/ PRIOR FILING DATE: 2000-12-27
/ NUMBER OF SEQ ID NOS: 133
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-2

Query Match          71.4% Score 15; DB 15; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
DB      8 GAACGTCGAGATGA 22

RESULT 70
US-10-033-243-12
/ Sequence 12, Application US/10033243
/ Publication No. US20030049266A1
/ GENERAL INFORMATION:
/ APPLICANT: FEARON, Karen L.
/ APPLICANT: DINA, Dino
/ TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
/ FILE REFERENCE: 37782001800
/ CURRENT APPLICATION NUMBER: US/10/033,243
/ CURRENT FILING DATE: 2002-04-03
/ PRIOR APPLICATION NUMBER: 60/258,675
/ PRIOR FILING DATE: 2000-12-27
/ NUMBER OF SEQ ID NOS: 133
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-12

Query Match          71.4% Score 15; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
/ NUMBER OF SEQ ID NOS: 133
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 22
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-22

Query Match          71.4% Score 15; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGTGAACGTTGCA 15
DB      1 TCGTGAACGTTGCA 15

RESULT 72
US-10-033-243-40
/ Sequence 40, Application US/10033243
/ Publication No. US20030049266A1
/ GENERAL INFORMATION:
/ APPLICANT: FEARON, Karen L.
/ APPLICANT: DINA, Dino
/ TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
/ FILE REFERENCE: 37782001800
/ CURRENT APPLICATION NUMBER: US/10/033,243
/ CURRENT FILING DATE: 2002-04-03
/ PRIOR APPLICATION NUMBER: 60/258,675
/ PRIOR FILING DATE: 2000-12-27
/ NUMBER OF SEQ ID NOS: 133
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 40
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-40

Query Match          71.4% Score 15; DB 15; Length 22;
Best Local Similarity 93.3%; Pred. No. 16;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGATGA 20
DB      8 GAACGTCGAGATGA 22

RESULT 73
US-10-033-243-45
/ Sequence 45, Application US/10033243
/ Publication No. US20030049266A1
/ GENERAL INFORMATION:
/ APPLICANT: FEARON, Karen L.
/ APPLICANT: DINA, Dino
/ TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
/ FILE REFERENCE: 37782001800
/ CURRENT APPLICATION NUMBER: US/10/033,243
/ CURRENT FILING DATE: 2002-04-03
/ PRIOR APPLICATION NUMBER: 60/258,675
/ PRIOR FILING DATE: 2000-12-27
/ NUMBER OF SEQ ID NOS: 133
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 45
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
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```
/ OTHER INFORMATION: Polynucleotide containing CG
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: 2..5
/ OTHER INFORMATION: n = 5-bromocytosine
US-10-033-243-45

Query Match
Best Local Similarity 71.4%; Score 15; DB 15; Length 22;
Matches 15; Conservative 100.0%; Pred. No. 16;
Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
   |||||
Db 8 GAACGTTGAGATGA 22

RESULT 74
US-10-033-243-46
/ Sequence 46, Application US/10033243
/ Publication No. US20030049266A1
/ GENERAL INFORMATION:
/ APPLICANT: FEARON, Karen L.
/ APPLICANT: DINA, Dino
/ TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
/ FILE REFERENCE: 37782001800
/ CURRENT APPLICATION NUMBER: US/10/033,243
/ PRIOR FILING DATE: 2002-04-03
/ PRIOR FILING DATE: 2000-12-27
/ NUMBER OF SEQ ID NOS: 133
/ SOFTWARE: FastSeq For Windows Version 4.0
/ SEQ ID NO 46
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Polynucleotide containing CG
/ NAME/KEY: misc_feature
/ LOCATION: 5
/ OTHER INFORMATION: n = 5-bromocytosine
US-10-033-243-46

Query Match
Best Local Similarity 71.4%; Score 15; DB 15; Length 22;
Matches 15; Conservative 100.0%; Pred. No. 16;
Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
   |||||
Db 8 GAACGTTGAGATGA 22

RESULT 75
US-10-033-243-59
/ Sequence 59, Application US/10033243
/ Publication No. US20030049266A1
/ GENERAL INFORMATION:
/ APPLICANT: FEARON, Karen L.
/ APPLICANT: DINA, Dino
/ TITLE OF INVENTION: IMMUNOMODULATORY POLYNUCLEOTIDES AND
/ FILE REFERENCE: 37782001800
/ CURRENT APPLICATION NUMBER: US/10/033,243
/ PRIOR FILING DATE: 2002-04-03
/ PRIOR FILING DATE: 2000-12-27
/ NUMBER OF SEQ ID NOS: 133
/ SOFTWARE: FastSeq For Windows Version 4.0
/ SEQ ID NO 59
/ LENGTH: 22
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Polynucleotide containing CG
US-10-033-243-59

Query Match
Best Local Similarity 71.4%; Score 15; DB 15; Length 22;
Matches 15; Conservative 100.0%; Pred. No. 16;
Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
   |||||
Db 8 GAACGTTGAGATGA 22
```

Search completed: December 17, 2003, 11:06:43
Job time : 1153 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2003, 09:15:24 : Search time 47 Seconds
(without alignments)
197.214 Million cell updates/sec

Title: US-10-033-243-132
Perfect score: 21
Sequence: 1 tcgcgcgaactcgcgatgat 21

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 569978 seqs, 220691566 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/1na/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/1na/5B.COMB.seq:*
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5: /cgn2_6/ptodata/1/1na/PCTUS.COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	ID	Description
1	15	71.4	22	4	US-09-235-742-19 Sequence 19, Appl
2	15	71.4	22	4	US-09-347-343-32 Sequence 32, Appl
3	15	71.4	22	4	US-09-820-484-1 Sequence 1, Appl
4	15	71.4	22	4	US-09-820-484-3 Sequence 3, Appl
5	15	71.4	22	4	US-09-774-403A-1 Sequence 1, Appl
6	14	66.7	816	3	US-08-776-251-10 Sequence 10, Appl
7	14	66.7	816	3	US-08-776-251-10 Sequence 10, Appl
8	14	66.7	4403765	3	US-09-103-840A-2 Sequence 2, Appl
9	14	66.7	4411529	3	US-09-103-840A-1 Sequence 1, Appl
10	13	61.9	321	3	US-09-060-756-260 Sequence 260, App
11	13	61.9	321	3	US-09-240-274-197 Sequence 197, App
12	13	61.9	321	4	US-09-670-314-260 Sequence 260, App
13	13	61.9	462	4	US-09-252-991A-16046 Sequence 16046, A
14	13	61.9	573	4	US-09-252-991A-9246 Sequence 9246, Ap
15	13	61.9	663	4	US-09-252-991A-9246 Sequence 9246, Ap
16	13	61.9	762	4	US-09-252-991A-16554 Sequence 16554, A
17	13	61.9	813	4	US-09-107-530A-1566 Sequence 1566, Ap
18	13	61.9	1221	4	US-09-252-991A-8921 Sequence 8921, Ap
19	13	61.9	1461	4	US-09-252-991A-9074 Sequence 9074, Ap
20	13	61.9	1545	4	US-09-252-991A-8710 Sequence 8710, Ap
21	13	61.9	1986	4	US-09-252-991A-16328 Sequence 16328, A
22	13	61.9	2091	4	US-09-252-991A-15954 Sequence 15954, A
23	13	61.9	43804	4	US-09-171-461-1 Sequence 1, Appl
24	12	57.1	20	4	US-09-286-098-11 Sequence 11, Appl
25	12	57.1	20	4	US-09-325-193A-91 Sequence 91, Appl
26	12	57.1	22	2	US-08-882-704A-18 Sequence 18, Appl
27	12	57.1	22	2	US-08-882-704A-18 Sequence 18, Appl

28	12	57.1	22	4	US-09-151-957-18 Sequence 18, Appl
29	12	57.1	22	4	US-09-151-957-18 Sequence 18, Appl
30	12	57.1	71	3	US-08-633-768A-12 Sequence 12, Appl
31	12	57.1	77	1	US-08-399-412A-58 Sequence 58, Appl
32	12	57.1	160	3	US-08-633-768A-14 Sequence 14, Appl
33	12	57.1	186	4	US-09-328-352-5855 Sequence 3855, Ap
34	12	57.1	212	4	US-09-313-294A-2448 Sequence 2448, Ap
35	12	57.1	268	4	US-09-313-294A-2857 Sequence 2857, Ap
36	12	57.1	283	4	US-09-313-294A-4896 Sequence 4896, Ap
37	12	57.1	288	4	US-09-252-991A-69 Sequence 69, Appl
38	12	57.1	378	4	US-09-252-991A-5259 Sequence 5259, Ap
39	12	57.1	406	3	US-09-060-756-563 Sequence 563, App
40	12	57.1	406	4	US-09-670-314-563 Sequence 563, App
41	12	57.1	432	4	US-09-252-991A-3530 Sequence 3530, Ap
42	12	57.1	441	4	US-09-252-991A-4565 Sequence 4565, Ap
43	12	57.1	658	3	US-08-861-774E-69 Sequence 69, Appl
44	12	57.1	806	4	US-09-198-119C-78 Sequence 78, Appl
45	12	57.1	813	4	US-09-107-532A-1566 Sequence 1566, Ap
46	12	57.1	830	4	US-09-198-119C-84 Sequence 84, Appl
47	12	57.1	906	4	US-09-252-991A-5994 Sequence 5994, Ap
48	12	57.1	981	4	US-09-252-991A-5231 Sequence 5231, Ap
49	12	57.1	1002	4	US-09-252-991A-3539 Sequence 3539, Ap
50	12	57.1	1009	4	US-09-091-097-37 Sequence 37, Appl
51	12	57.1	1038	4	US-09-252-991A-16116 Sequence 16116, A
52	12	57.1	1038	4	US-09-252-991A-16116 Sequence 16116, A
53	12	57.1	1113	1	US-08-229-287-1 Sequence 1, Appl
54	12	57.1	1119	4	US-09-252-991A-6391 Sequence 6391, Ap
55	12	57.1	1303	2	US-08-793-410-11 Sequence 11, Appl
56	12	57.1	1362	4	US-09-328-352-943 Sequence 943, App
57	12	57.1	1368	4	US-09-252-991A-64 Sequence 64, Appl
58	12	57.1	1443	4	US-09-252-991A-6308 Sequence 6308, Ap
59	12	57.1	1578	4	US-09-351-224E-7 Sequence 7, Appl
60	12	57.1	1578	4	US-09-677-468A-7 Sequence 7, Appl
61	12	57.1	1578	4	US-09-677-468A-7 Sequence 7, Appl
62	12	57.1	1644	4	US-09-252-991A-3548 Sequence 3548, Ap
63	12	57.1	1764	4	US-09-351-224E-6 Sequence 6, Appl
64	12	57.1	1764	4	US-09-677-468A-6 Sequence 6, Appl
65	12	57.1	1764	4	US-09-677-468A-6 Sequence 6, Appl
66	12	57.1	1836	4	US-07-754-918A-1 Sequence 1, Appl
67	12	57.1	1900	1	US-09-555-000-1 Sequence 1, Appl
68	12	57.1	2058	1	US-08-358-117-1 Sequence 1, Appl
69	12	57.1	2058	3	US-08-470-588-1 Sequence 1, Appl
70	12	57.1	2426	3	US-08-528-026C-3 Sequence 3, Appl
71	12	57.1	2595	4	US-09-221-017B-225 Sequence 225, App
72	12	57.1	2595	4	US-09-619-353-13 Sequence 13, Appl
73	12	57.1	2760	4	US-09-221-017B-462 Sequence 462, App
74	12	57.1	2832	4	US-09-252-991A-3523 Sequence 3523, Ap
75	12	57.1	2854	4	US-08-936-165A-66 Sequence 66, Appl
76	12	57.1	3664	4	US-07-880-913-1 Sequence 1, Appl
77	12	57.1	3872	5	PCT-US93-12169-1 Sequence 1, Appl
78	12	57.1	5648	3	US-09-371-008-1 Sequence 1, Appl
79	12	57.1	6909	4	US-09-199-637A-111 Sequence 11, App
80	12	57.1	7527	4	US-09-252-991A-71 Sequence 11, Appl
81	12	57.1	12566	4	US-08-961-527-149 Sequence 149, App
82	12	57.1	13825	4	US-09-634-238-29 Sequence 29, Appl
83	12	57.1	35412	4	US-08-311-721A-132 Sequence 132, App
84	12	57.1	71989	4	US-09-443-501A-2 Sequence 2, Appl
85	12	57.1	536165	4	US-09-214-808-1 Sequence 1, Appl
86	12	57.1	1830121	4	US-09-557-884-1 Sequence 1, Appl
87	12	57.1	1830121	4	US-09-557-884-1 Sequence 1, Appl
88	12	57.1	1830121	4	US-09-643-990A-1 Sequence 1, Appl
89	12	57.1	1830121	4	US-09-643-990A-1 Sequence 1, Appl
90	12	57.1	4403765	3	US-09-103-840A-2 Sequence 2, Appl
91	12	57.1	4411529	3	US-09-103-840A-1 Sequence 1, Appl
92	11	52.4	21	4	US-09-374-168-62 Sequence 62, Appl
93	11	52.4	22	4	US-09-797-403A-2 Sequence 2, Appl
94	11	52.4	24	1	US-08-064-271-9 Sequence 9, Appl
95	11	52.4	24	3	US-08-930-589A-9 Sequence 9, Appl
96	11	52.4	24	3	US-09-599-781-9 Sequence 9, Appl
97	11	52.4	26	4	US-09-322-409-153 Sequence 153, App
98	11	52.4	26	4	US-09-451-527-153 Sequence 153, App
99	11	52.4	39	1	US-08-293-892-1 Sequence 1, Appl
100	11	52.4	39	1	US-08-459-890-1 Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-09-235-742-19
; Sequence 19, Application US/09235742
; Patent No. 6498148
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; TITLE OF INVENTION: Immunization-Free Methods for Treating
; TITLE OF INVENTION: Antigen-Stimulated Inflammation in a Mammalian Host and
; TITLE OF INVENTION: Shifting the Host's Antigen Immune Responsiveness to a TH1
; FILE REFERENCE: 6510-170CON4
; CURRENT APPLICATION NUMBER: US/09/235,742
; CURRENT FILING DATE: 1999-01-21
; EARLIER APPLICATION NUMBER: 08/927,120
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 08/593,554
; EARLIER FILING DATE: 1996-01-30
; EARLIER APPLICATION NUMBER: 08/725,968
; EARLIER FILING DATE: 1996-10-04
; EARLIER APPLICATION NUMBER: 60/028,118
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant or Synthetic Sequence
US-09-235-742-19

Query Match

Best Local Similarity 71.4%; Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||
DB 8 GAACGTTGAGATGA 22

RESULT 2

US-09-347-343-32
; Sequence 32, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 22
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-32

Query Match

Best Local Similarity 71.4%; Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||
DB 8 GAACGTTGAGATGA 22

RESULT 3

US-09-820-484-1
; Sequence 1, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188US1
; CURRENT APPLICATION NUMBER: US/09/820,484
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Disulfide-linked phosphorothioate ISS-ODN
; NAME/KEY: modified base
; LOCATION: (1)...(1)
; OTHER INFORMATION: disulfide thymine
US-09-820-484-1

Query Match

Best Local Similarity 71.4%; Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGATGA 20
|||
DB 8 GAACGTTGAGATGA 22

RESULT 4

US-09-820-484-3
; Sequence 3, Application US/09820484
; Patent No. 6534062
; GENERAL INFORMATION:
; APPLICANT: Raz, Eyal
; APPLICANT: Cho, Hearn Jay
; APPLICANT: Richman, Douglas
; APPLICANT: Horner, Anthony A.
; TITLE OF INVENTION: Method for Increasing a Cytotoxic T
; TITLE OF INVENTION: Lymphocyte Response in vivo.
; FILE REFERENCE: 06510-188US1
; CURRENT APPLICATION NUMBER: US/09/820,484
; CURRENT FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/192,537
; PRIOR FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: US 60/203,567
; PRIOR FILING DATE: 2000-05-11
; PRIOR APPLICATION NUMBER: US 60/215,895
; PRIOR FILING DATE: 2000-07-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: phosphorothioate ISS-ODN
US-09-820-484-3

Query Match

71.4%; Score 15; DB 4; Length 22;

Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

RESULT 5

US-09-774-403A-1
; Sequence 1, Application US/09774403A
; Patent No. 6552006
; GENERAL INFORMATION:
; APPLICANT: Eval Raz
; APPLICANT: Richard Kornbluth
; APPLICANT: Antonio Catanzaro
; APPLICANT: Tomoko Hayashi
; APPLICANT: Dennis Carson
; TITLE OF INVENTION: Immunomodulatory Polynucleotides in
; TITLE OF INVENTION: Treatment of Infection by an Intracellular Pathogen
; FILE REFERENCE: UCA1166
; CURRENT APPLICATION NUMBER: US/09/774,403A
; CURRENT FILING DATE: 2002-04-15
; PRIOR APPLICATION NUMBER: 60/179,353
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Immunomodulatory sequence
US-09-774-403A-1

Query Match 71.4%; Score 15; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACGTCGAGATGA 20
Db 8 GAACGTCGAGATGA 22

RESULT 6

US-08-776-251-10
; Sequence 10, Application US/08776251
; Patent No. 6025340
; GENERAL INFORMATION:
; APPLICANT: Springer, Caroline J
; APPLICANT: Marais, Richard
; TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6025340th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,251
; FILING DATE: 31-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01782
; FILING DATE: 27-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9415167.7
; FILING DATE: 27-JUL-1994

ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 620-20
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-776-251-10

US-08-776-251-10

Query Match 66.7%; Score 14; DB 3; Length 816;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTCGAGA 17
Db 619 TCGAACGTCGAGA 632

RESULT 7

US-08-776-251-10/c
; Sequence 10, Application US/08776251
; Patent No. 6025340
; GENERAL INFORMATION:
; APPLICANT: Springer, Caroline J
; APPLICANT: Marais, Richard
; TITLE OF INVENTION: Surface expression of enzyme in gene directed prodrug therapy
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye
; STREET: 1100 No. 6025340th Glebe Road, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/776,251
; FILING DATE: 31-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01782
; FILING DATE: 27-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9415167.7
; FILING DATE: 27-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Arthur R. Crawford
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 620-20
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-776-251-10

Query Match 66.7%; Score 14; DB 3; Length 816;
Best Local Similarity 100.0%; Pred. No. 6.5;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTCGAGA 17
Db 801 TCGAACGTCGAGA 788

```
RESULT 8
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          66.7%; Score 14; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGTGAACGTTG 14
      |||||
Db      735047 TCGTGAACGTTG 735034

RESULT 9
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          66.7%; Score 14; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TCGTGAACGTTG 14
      |||||
Db      733615 TCGTGAACGTTG 733602

RESULT 10
US-09-060-756-260
; Sequence 260, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
```

```
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 260
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (various positions within the sequence)
; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-260

Query Match          61.9%; Score 13; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACGTTGAGATGA 20
      |||||
Db      75 ACGTTGAGATGA 87

RESULT 11
US-09-240-274-197/c
; Sequence 197, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: RH(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEROOF
; FILE REFERENCE: 09596-4202
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 197
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH8
US-09-240-274-197

Query Match          61.9%; Score 13; DB 3; Length 321;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGAAGTTGAGA 17
      |||||
Db      292 CGAAGTTGAGA 280

RESULT 12
US-09-670-314-260
; Sequence 260, Application US/09670314
; Patent No. 6492506
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
```


;; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
;; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
;; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
;; FILE REFERENCE: 3495-0169
;; CURRENT APPLICATION NUMBER: US/09/670,314
;; CURRENT FILING DATE: 2001-01-12
;; PRIOR APPLICATION NUMBER: 09/060,756
;; PRIOR FILING DATE: 1998-04-16
;; NUMBER OF SEQ ID NOS: 743
;; SOFTWARE: Patent In Ver. 2.0
;; SEQ ID NO 260
;; LENGTH: 321
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (various positions within the sequence)
;; OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-260

Query Match 61.9%; Score 13; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACCTTCGAGATCA 20
Db 75 ACCTTCGAGATCA 87

RESULT 13
US-09-252-991A-16046
; Sequence 16046, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16046
; LENGTH: 462
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16046

Query Match 61.9%; Score 13; DB 4; Length 462;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACCTTCGAGATCA 20
Db 34 ACCTTCGAGATCA 46

RESULT 14
US-09-252-991A-9162/c
; Sequence 9162, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18

;; PRIOR APPLICATION NUMBER: US 60/094,190
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 9162
;; LENGTH: 573
;; TYPE: DNA
;; ORGANISM: Pseudomonas aeruginosa
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: (117)
;; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-9162

Query Match 61.9%; Score 13; DB 4; Length 573;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACCTTCGAGAT 18
Db 286 GAACCTTCGAGAT 274

RESULT 15
US-09-252-991A-9246/c
; Sequence 9246, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9246
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9246

Query Match 61.9%; Score 13; DB 4; Length 663;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GAACCTTCGAGAT 18
Db 45 GAACCTTCGAGAT 33

RESULT 16
US-09-252-991A-16554/c
; Sequence 16554, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16554
; LENGTH: 762
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16554

Query Match 61.9%; Score 13; DB 4; Length 762;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ACCTTCGAGATCA 20
|||||
DB 555 ACCTTCGAGATCA 543

RESULT 17

US-09-107-532A-1566
; Sequence 1566, Application US/09107532A
; Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Atinello, Pamela Deneka

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-8277

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 1566:

SEQUENCE CHARACTERISTICS:

LENGTH: 813 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc.feature

LOCATION: (B) LOCATION 1...813

SEQUENCE DESCRIPTION: SEQ ID NO: 1566:

US-09-107-532A-1566

Query Match 61.9%; Score 13; DB 4; Length 813;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTCGAACGTTTCA 15
|||||
DB 241 GTCGAACGTTTCA 253

RESULT 18

US-09-252-991A-8921
; Sequence 8921, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 8921

LENGTH: 1221

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

FEATURE:

NAME/KEY: unsure

LOCATION: (458)

OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-252-991A-8921

Query Match 61.9%; Score 13; DB 4; Length 1221;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGAT 18
|||||
DB 189 GAACGTTGAGAT 201

RESULT 19

US-09-252-991A-9074/C
; Sequence 9074, Application US/09252991A
; Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 9074

LENGTH: 1461

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

FEATURE:

NAME/KEY: unsure

LOCATION: (951),(1078)

OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.

US-09-252-991A-9074

Query Match 61.9%; Score 13; DB 4; Length 1461;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GAACGTTGAGAT 18
|||||
DB 212 GAACGTTGAGAT 200

RESULT 20

US-09-252-991A-8710
; Sequence 8710, Application US/09252991A

```
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 8710
; LENGTH: 1545
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (760)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-252-991A-8710

Query Match      61.9%; Score 13; DB 4; Length 1545;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GACGCTCGAGAT 18
      |||||
Db      491 GACGCTCGAGAT 503

RESULT 21
US-09-252-991A-16328/c
; Sequence 16328, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16328
; LENGTH: 1986
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16328

Query Match      61.9%; Score 13; DB 4; Length 1986;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACGTTCGAGATGA 20
      |||||
Db      1676 ACGTTCGAGATGA 1664

RESULT 22
US-09-252-991A-15954
; Sequence 15954, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
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; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15954
; LENGTH: 2091
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15954

Query Match      61.9%; Score 13; DB 4; Length 2091;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 ACGTTCGAGATGA 20
      |||||
Db      473 ACGTTCGAGATGA 485

RESULT 23
US-09-171-461-1
; Sequence 1, Application US/09171461
; Patent No. 6335016
; GENERAL INFORMATION:
; APPLICANT: Baker, Adam
; APPLICANT: Cotten, Matthew
; APPLICANT: Chioda, Susanna
; APPLICANT: Kuzbauer, Robert
; APPLICANT: Schaffner, Gotthold
; TITLE OF INVENTION: Chicken Embryo Lethal Orphan (CELO) Virus
; FILE REFERENCE: 0652.1800000
; CURRENT APPLICATION NUMBER: US/09/171,461
; CURRENT FILING DATE: 1999-01-12
; EARLIER APPLICATION NUMBER: PCT/EP97/01944
; PRIOR FILING DATE: 1997-04-18
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 43804
; TYPE: DNA
; ORGANISM: CELO Virus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (12193)..(15043)
; OTHER INFORMATION: /gene: L1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15080)
; OTHER INFORMATION: /note= L2 region penton base splice acceptor site
; FEATURE:
; NAME/KEY: gene
; LOCATION: (15110)..(17495)
; OTHER INFORMATION: /gene: L2
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: (17526)
; FEATURE:
; NAME/KEY: gene
; LOCATION: (17559)..(21754)
; OTHER INFORMATION: /gene: L3
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21102)
; OTHER INFORMATION: /gene: L3 /note= hexon splice acceptor site
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (21123)
```

```
OTHER INFORMATION: /gene: l3 /note= protease splice acceptor site
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21767)
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21824)
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21836)
FEATURE:
NAME/KEY: polyA_site
LOCATION: (21882)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23608)
OTHER INFORMATION: /note= 100k splice acceptor site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (23649)
OTHER INFORMATION: /note= 100k splice acceptor site
FEATURE:
NAME/KEY: gene
LOCATION: (23680)..(27886)
OTHER INFORMATION: /gene: L4
FEATURE:
NAME/KEY: polyA_site
LOCATION: (27920)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28315)
OTHER INFORMATION: /note= fibre splice acceptor site
FEATURE:
NAME/KEY: misc_feature
LOCATION: (28351)
OTHER INFORMATION: / note= fibre splice acceptor site
FEATURE:
NAME/KEY: gene
LOCATION: (28363)..(31768)
OTHER INFORMATION: /gene: L5
FEATURE:
NAME/KEY: misc_feature
LOCATION: (30511)
OTHER INFORMATION: /gene: L5
FEATURE:
NAME/KEY: polyA_site
LOCATION: (31770)
US-09-171-461-1

Query Match          61.9%; Score 13; DB 4; Length 43804;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGAT 18
      |||||
Db      25862 GAACGTCGAGAT 25874

RESULT 24
US-09-286-098-11/c
; Sequence 11, Application US/09286098
; Patent No. 6218371
; GENERAL INFORMATION:
; APPLICANT: Kriegl, Arthur M.
; TITLE OF INVENTION: Methods and Products for Stimulating the
; TITLE OF INVENTION: Immune System Using Immunotherapeutic Oligonucleotides and
; FILE REFERENCE: C1039/7026/HCL
; CURRENT APPLICATION NUMBER: US/09/286,098
; CURRENT FILING DATE: 1999-04-02
; EARLIER APPLICATION NUMBER: US 60/080,729
; EARLIER FILING DATE: 1998-04-03
```

```
NUMBER OF SEQ ID NOS: 105
SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Sequence
US-09-286-098-11

Query Match          57.1%; Score 12; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGA 17
      |||||
Db      18 GAACGTCGAGA 7

RESULT 25
US-09-325-193A-91/c
; Sequence 91, Application US/09325193A
; Patent No. 6406705
; GENERAL INFORMATION:
; APPLICANT: Davis, Heather L.
; APPLICANT: Schorr, Joachim
; APPLICANT: Kriegl, Arthur M.
; TITLE OF INVENTION: Use of Nucleic Acids Containing
; TITLE OF INVENTION: Unmethylated CpG Dinucleotide as an Adjuvant
; FILE REFERENCE: C1039/7025/HCL
; CURRENT APPLICATION NUMBER: US/09/325,193A
; CURRENT FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: US 09/154,614
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: PCT/US98/04703
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 60/040,376
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 91
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Oligonucleotide
US-09-325-193A-91

Query Match          57.1%; Score 12; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTCGAGA 17
      |||||
Db      18 GAACGTCGAGA 7

RESULT 26
US-08-882-704A-18
; Sequence 18, Application US/08882704A
; Patent No. 5879906
; GENERAL INFORMATION:
; APPLICANT: Jefferson, Richard A.
; APPLICANT: Wilson, Katherine J.
; APPLICANT: Leader, Michael
; TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6100 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
```

ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,704A
FILING DATE: 25-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5879906tendburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-882-704A-18

Query Match 57.1%; Score 12; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTGCA 15
|||
Db 8 TCGAACGTTGCA 19

RESULT 27
US-08-882-704A-18/c
Sequence 18, Application US/08882704A
Patent No. 5879906
GENERAL INFORMATION:
APPLICANT: Jefferson, Richard A.
APPLICANT: Wilson, Katherine J.
APPLICANT: Leader, Michael
TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,704A
FILING DATE: 25-JUN-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: No. 5879906tendburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-882-704A-18

Query Match 57.1%; Score 12; DB 2; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTGCA 15
|||
Db 19 TCGAACGTTGCA 8

RESULT 28
US-09-151-957-18
Sequence 18, Application US/09151957
Patent No. 6429292
GENERAL INFORMATION:
APPLICANT: Jefferson, Richard A.
APPLICANT: Wilson, Katherine J.
APPLICANT: Leader, Michael
TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,957
FILING DATE: 11-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/882,704
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6429292tendburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 622-4900
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-151-957-18

Query Match 57.1%; Score 12; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAACGTTGCA 15
|||
Db 8 TCGAACGTTGCA 19

RESULT 29
US-09-151-957-18/c
Sequence 18, Application US/09151957
Patent No. 6429292
GENERAL INFORMATION:
APPLICANT: Jefferson, Richard A.
APPLICANT: Wilson, Katherine J.
APPLICANT: Leader, Michael

TITLE OF INVENTION: GLUCURONIDE REPRESSORS AND USES THEREOF
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/151,957
FILING DATE: 11-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/882,704
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: No. 6429292lenburg Ph.D., Carol
REGISTRATION NUMBER: 39,317
REFERENCE/DOCKET NUMBER: 190106.404
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-151-957-18

Query Match 57.1%; Score 12; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TCGAAGCTTGA 15
|||||
Db 19 TCGAAGCTTGA 8

RESULT 30
US-08-633-768A-12/c
Sequence 12, Application US/08633768A
Patent No. 6013504
GENERAL INFORMATION:
APPLICANT: YU, SHUKUN
APPLICANT: BOJSEN, KIRSTEN
APPLICANT: KRAGH, KARSTEN
APPLICANT: BOJKO, MAJA
APPLICANT: NIELSEN, JOHN
APPLICANT: MARCUSEN, JAN
TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM
TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knodde, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/633,768A
FILING DATE: 02-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 9321301.5
FILING DATE: 15-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: DY0U7.001APC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 71 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
US-08-633-768A-12

Query Match 57.1%; Score 12; DB 3; Length 71;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGCTTGAG 16
|||||
Db 26 CGAAGCTTGAG 15

RESULT 31
US-08-399-412A-58/c
Sequence 58, Application US/08399412A
Patent No. 5622828
GENERAL INFORMATION:
APPLICANT: Palma, David
APPLICANT: Gold, Larry
TITLE OF INVENTION: High-Affinity Oligonucleotide
TITLE OF INVENTION: Ligands to Secretory Phospholipase
TITLE OF INVENTION: A2 (sPLA2)
NUMBER OF SEQUENCES: 122
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: MotifPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/399,412A
FILING DATE: 6-MARCH-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Julie L. Bernard
REGISTRATION NUMBER: 36,450
REFERENCE/DOCKET NUMBER: NEX27

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 58:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 77 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-399-412A-58

Query Match 57.1%; Score 12; DB 1; Length 77;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTGCAAGCTTCG 14
 |||||
 DB 59 GTGCAAGCTTCG 48

RESULT 32

US-08-633-768A-14/c
 Sequence 14, Application US/08633768A
 Patent No. 6013504

GENERAL INFORMATION:
 APPLICANT: YU, SHUKUN
 BOUSSEY, KIRSTEN
 APPLICANT: KRAIG, KARSTEN
 APPLICANT: BOJKO, MAJIA
 APPLICANT: NIELSEN, JOHN
 APPLICANT: MARCUSSEN, JAN
 TITLE OF INVENTION: ALPHA-1,4-GLUCAN LYASE FROM
 TITLE OF INVENTION: A FUNGUS INFECTED ALGAE, ITS PURIFICATION
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Knobbe, Martens, Olson & Bear
 STREET: 620 Newport Center Drive 16th Floor
 CITY: Newport Beach
 STATE: CA
 COUNTRY: U.S.A.
 ZIP: 92660
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FaasSEQ Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/633,768A
 FILING DATE: 02-JUL-1996
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 9321301.5
 FILING DATE: 15-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Altman, Daniel E
 REGISTRATION NUMBER: 34,115
 REFERENCE/DOCKET NUMBER: DYOU7.001APC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 714-760-0404
 TELEFAX: 714-760-9502
 TELEX:
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 160 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Genomic DNA
 US-08-633-768A-14

Query Match 57.1%; Score 12; DB 3; Length 160;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGTTCGAG 16
 |||||
 DB 26 CGAAGTTCGAG 15

RESULT 33
 US-09-328-352-3855/c
 Sequence 3855, Application US/09328352
 Patent No. 6562958

GENERAL INFORMATION:
 APPLICANT: Gary L. Breton et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 TITLE OF INVENTION: BAUMANNIT FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: GTC99-03PA
 CURRENT APPLICATION NUMBER: US/09/328,352
 CURRENT FILING DATE: 1999-06-04
 NUMBER OF SEQ ID NOS: 8252
 SEQ ID NO 3855
 LENGTH: 186
 TYPE: DNA
 ORGANISM: Acinetobacter baumannii
 US-09-328-352-3855

Query Match 57.1%; Score 12; DB 4; Length 186;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21
 |||||
 DB 98 GTTCGAGATGAT 87

RESULT 34

US-09-313-294A-2448
 Sequence 2448, Application US/09313294A
 Patent No. 6476212

GENERAL INFORMATION:
 APPLICANT: Laljundi, Raghunath V.
 APPLICANT: Ito, Laura Y.
 APPLICANT: Sherman, Bradley K.
 TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 FILE REFERENCE: PL-0017 US
 CURRENT APPLICATION NUMBER: US/09/313,294A
 CURRENT FILING DATE: 1999-05-14
 NUMBER OF SEQ ID NOS: 7600
 SOFTWARE: PERL Program
 SEQ ID NO 2448
 LENGTH: 212
 TYPE: DNA
 ORGANISM: Zea mays
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Incyte ID No. 6476212 700552684H1
 US-09-313-294A-2448

Query Match 57.1%; Score 12; DB 4; Length 212;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21
 |||||
 DB 9 GTTCGAGATGAT 20

RESULT 35

US-09-313-294A-2857
 Sequence 2857, Application US/09313294A
 Patent No. 6476212

GENERAL INFORMATION:
 APPLICANT: Laljundi, Raghunath V.
 APPLICANT: Ito, Laura Y.
 APPLICANT: Sherman, Bradley K.

```

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 2857
; LENGTH: 268
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700553386H1
; NAME/KEY: unsure
; LOCATION: 257
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-2857

Query Match          57.1%; Score 12; DB 4; Length 268;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GTTCGAGATGAT 21
Db      132 GTTCGAGATGAT 143

RESULT 36
; Sequence 4896, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalagudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4896
; LENGTH: 283
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700349228H1
; NAME/KEY: unsure
; LOCATION: 122, 140
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4896

Query Match          57.1%; Score 12; DB 4; Length 283;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GAACGTTGAGA 17
Db      100 GAACGTTGAGA 89

RESULT 37
US-09-252-991A-69
; Sequence 69, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
```

```

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 69
; LENGTH: 288
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-69

Query Match          57.1%; Score 12; DB 4; Length 288;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 CGAACGTCGAG 16
Db      83 CGAACGTCGAG 94

RESULT 38
US-09-252-991A-5259/c
; Sequence 5259, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5259
; LENGTH: 378
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5259

Query Match          57.1%; Score 12; DB 4; Length 378;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 GTCGAACGTCG 14
Db      27 GTCGAACGTCG 16

RESULT 39
US-09-060-756-563
; Sequence 563, Application US/09060756
; Patent No. 6183957
; GENERAL INFORMATION:
; APPLICANT: Cole, Stewart
; APPLICANT: Buchrieser-Brosch, Roland
; APPLICANT: Gordon, Stephen
; APPLICANT: Billault, Alain
; TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
; TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
; TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
; FILE REFERENCE: 3495-0169
; CURRENT APPLICATION NUMBER: US/09/060,756
; CURRENT FILING DATE: 1998-04-16
; NUMBER OF SEQ ID NOS: 743
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 563
; LENGTH: 406
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
```


NAME/KEY: unsure
LOCATION: (various positions within the sequence)
OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-060-756-563

Query Match 57.1%; Score 12; DB 3; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTCGAACGTTTCG 14
|||||
DB 287 GTCGAACGTTTCG 298

RESULT 40
US-09-670-314-563
Sequence 563, Application US/09670314
Patent No. 6492506
GENERAL INFORMATION:
APPLICANT: Cole, Stewart
APPLICANT: Buchrieser-Brosch, Roland
APPLICANT: Gordon, Stephen
APPLICANT: Billault, Alain
TITLE OF INVENTION: METHOD FOR ISOLATING A POLYNUCLEOTIDE OF INTEREST FROM
TITLE OF INVENTION: THE GENOME OF A MYCOBACTERIUM USING A BAC-BASED DNA
TITLE OF INVENTION: LIBRARY APPLICATION TO THE DETECTION OF MYCOBACTERIA
FILE REFERENCE: 3495-0169
CURRENT APPLICATION NUMBER: US/09/670,314
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: 09/060,756
PRIOR FILING DATE: 1998-04-16
NUMBER OF SEQ ID NOS: 743
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 563
LENGTH: 406
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
FEATURE:
NAME/KEY: unsure
LOCATION: (various positions within the sequence)
OTHER INFORMATION: applicants are uncertain of bases designated as "n"
US-09-670-314-563

Query Match 57.1%; Score 12; DB 4; Length 406;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GTCGAACGTTTCG 14
|||||
DB 287 GTCGAACGTTTCG 298

RESULT 41
US-09-252-991A-3530
Sequence 3530, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 3530
LENGTH: 432
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3530

Query Match 57.1%; Score 12; DB 4; Length 432;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20
|||||
DB 421 CGTTCGAGATGA 432

RESULT 42
US-09-252-991A-4565
Sequence 4565, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4565
LENGTH: 441
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4565

Query Match 57.1%; Score 12; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21
|||||
DB 55 GTTCGAGATGAT 66

RESULT 43
US-08-861-774E-69/C
Sequence 69, Application US/08861774E
Patent No. 6287007
GENERAL INFORMATION:
APPLICANT: Waters, Barbara
APPLICANT: Miao, Vivian
APPLICANT: Ho, Yap
APPLICANT: Tong, Seow
TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
TITLE OF INVENTION: BIOACTIVE MOLECULES
FILE REFERENCE: 9993-006
CURRENT APPLICATION NUMBER: US/08/861,774E
CURRENT FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 94
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 69
LENGTH: 658
TYPE: DNA
ORGANISM: Ureua florida
US-08-861-774E-69

Query Match 57.1%; Score 12; DB 3; Length 658;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21
|||||
DB 187 GTTCGAGATGAT 176

RESULT 44

US-09-198-119C-78
; Sequence 78, Application US/09198119C
; Patent No. 6417428
; GENERAL INFORMATION:
; APPLICANT: Thomashow, Michael
; APPLICANT: Stockinger, Eric
; APPLICANT: Jaglo-Otlesen, Kirsten
; APPLICANT: Gilmour, Sarah
; APPLICANT: Zarka, Daniel
; APPLICANT: Jiang, Cai-zhong
; TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance
; FILE REFERENCE: 19117.713 Seq List
; CURRENT APPLICATION NUMBER: US/09/198,119C
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 08/706,270
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/018,233
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/017,816
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,235
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/017,575
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,227
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,234
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 78
; LENGTH: 806
; TYPE: DNA
; ORGANISM: Brassica rapa
; FEATURE:
; OTHER INFORMATION: brcBF3 gene
US-09-198-119C-78

Query Match 57.1%; Score 12; DB 4; Length 806;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACGTTCGAGATG 19
|||
Db 692 ACGTTCGAGATG 703

RESULT 45
US-09-107-532A-1566/C
; Sequence 1566, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781) 893-5007
TELEFAX: (781) 893-8277
INFORMATION FOR SEQ ID NO: 1566:
SEQUENCE CHARACTERISTICS:
LENGTH: 813 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...813
SEQUENCE DESCRIPTION: SEQ ID NO: 1566:
US-09-107-532A-1566

Query Match 57.1%; Score 12; DB 4; Length 813;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TCGAAGTTTCA 15
|||
Db 253 TCGAAGTTTCA 242

RESULT 46
US-09-198-119C-84
; Sequence 84, Application US/09198119C
; Patent No. 6417428
; GENERAL INFORMATION:
; APPLICANT: Thomashow, Michael
; APPLICANT: Stockinger, Eric
; APPLICANT: Jaglo-Otlesen, Kirsten
; APPLICANT: Gilmour, Sarah
; APPLICANT: Zarka, Daniel
; APPLICANT: Jiang, Cai-zhong
; TITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance
; FILE REFERENCE: 19117.713 Seq List
; CURRENT APPLICATION NUMBER: US/09/198,119C
; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: US 08/706,270
; PRIOR FILING DATE: 1998-09-04
; PRIOR APPLICATION NUMBER: US 09/018,233
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/017,816
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,235
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/017,575
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,227
; PRIOR FILING DATE: 1998-02-03
; PRIOR APPLICATION NUMBER: US 09/018,234
; PRIOR FILING DATE: 1998-02-03
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 84
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Brassica rapa
; FEATURE:
; OTHER INFORMATION: brcBF6 gene

US-09-198-119C-84

Query Match

Best Local Similarity 57.1%; Score 12; DB 4; Length 830;
Matches 12; Conservativity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;

QY 8 ACCTCGAGATG 19

DB 696 ACCTCGAGATG 707

RESULT 47

US-09-252-991A-5994

Sequence 5994, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 5994

LENGTH: 906

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-5994

Query Match

Best Local Similarity 57.1%; Score 12; DB 4; Length 906;
Matches 12; Conservativity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21

DB 237 GTTCGAGATGAT 248

RESULT 48

US-09-252-991A-5231/C

Sequence 5231, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 5231

LENGTH: 981

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-5231

Query Match

Best Local Similarity 57.1%; Score 12; DB 4; Length 981;
Matches 12; Conservativity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;

QY 3 GTCGAAGCTTCG 14

DB 22 GTCGAAGCTTCG 11

RESULT 49

US-09-252-991A-3539

Sequence 3539, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 3539

LENGTH: 1002

TYPE: DNA

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-3539

Query Match

Best Local Similarity 57.1%; Score 12; DB 4; Length 1002;
Matches 12; Conservativity 100.0%; Pred. No. 1e+02; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20

DB 717 CGTTCGAGATGA 728

RESULT 50

US-09-091-097-37/C

Sequence 37, Application US/09091097

Patent No. 6432407

GENERAL INFORMATION:

APPLICANT: TAKESAKO, KAZUTOH

APPLICANT: YAGIHARA, TOMOKO

APPLICANT: KURODA, MASANOBU

APPLICANT: ONISHI, YOSHIMI

APPLICANT: KATO, IKUNOSHIN

APPLICANT: AKIYAMA, KAZUO

APPLICANT: YASUEDA, HIROSHI

APPLICANT: YAMAGUCHI, HIDEYO

TITLE OF INVENTION: ANTIGENIC PROTEIN ORIGINATING IN

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESS: BIRCH, STEWART, KOLASCH & BIRCH, LLP

STREET: PO BOX 747

CITY: FALLS CHURCH

STATE: VA

COUNTRY: USA

ZIP: 22040-0747

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/091,097

FILING DATE:

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: WEINER, MARC S.

REGISTRATION NUMBER: 32,181

REFERENCE/DOCKET NUMBER: 1422-0346P

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-205-8050

TELEFAX: 703-205-8050

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 1009 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-09-091-097-37

Query Match 57.1%; Score 12; DB 4; Length 1009;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGA 21
|||||
Db 306 GTTCGAGATGA 295

RESULT 51
US-09-252-991A-16116/c
Sequence 16116, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16116
LENGTH: 1038
TYPE: DNA

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16116

Query Match 57.1%; Score 12; DB 4; Length 1038;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20
|||||
Db 920 CGTTCGAGATGA 909

RESULT 52
US-09-252-991A-16487
Sequence 16487, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 16487
LENGTH: 1038
TYPE: DNA

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16487

Query Match 57.1%; Score 12; DB 4; Length 1038;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20
|||||
Db 374 CGTTCGAGATGA 385

RESULT 53
US-08-229-287-1/c

Sequence 1, Application US/08229287
Patent No. 5530193

GENERAL INFORMATION:
APPLICANT: Clark Jr., John M.
APPLICANT: Jilka, Joseph M.
APPLICANT: Murry, Lynn E.
APPLICANT: Scarafia, Liliana E.
TITLE OF INVENTION: VIRUS RESISTANT CORN PLANTS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sandoz Agro, Inc.
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/229,287
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/067,257
FILING DATE: 25-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/817,922
FILING DATE: 08-JAN-1992

ATTORNEY/AGENT INFORMATION:
NAME: Marcus-Wyner, Lynn
REGISTRATION NUMBER: 34,869
REFERENCE/DOCKET NUMBER: 135-1084/XCC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/354-3588
TELEFAX: 415/857-1125
INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1113 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: 1..876

US-08-229-287-1

Query Match 57.1%; Score 12; DB 1; Length 1113;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGA 21
|||||
Db 695 GTTCGAGATGA 684

RESULT 54

US-09-252-991A-6391/c
Sequence 6391, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 6391
LENGTH: 1119
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6391

Query Match 57.1%; Score 12; DB 4; Length 1119;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21
|||||
DB 1095 GTTCGAGATGAT 1084

RESULT 55
US-08-793-410-11/c
Sequence 11, Application US/08793410
Patent No. 5955650

GENERAL INFORMATION:
APPLICANT: HITZ, WILLIAM DEAN
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF CANOLA
TITLE OF INVENTION: AND SOYBEAN PALMITOYL-ACP THIO-
TITLE OF INVENTION: ESTERASE GENES AND THEIR USE IN
TITLE OF INVENTION: THE REGULATION OF FATTY ACID
TITLE OF INVENTION: AND CANOLA PLANTS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
ZIP: 19898

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/793,410
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10627
FILING DATE: AUGUST 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNN M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: CR-9567-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-793-410-11

Query Match 57.1%; Score 12; DB 2; Length 1303;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AACGTTGAGAT 18
|||||
DB 23 AACGTTGAGAT 12

RESULT 56
US-09-328-352-943
Sequence 943, Application US/09328352
Patent No. 6562958

GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 943
LENGTH: 1362
TYPE: DNA

ORGANISM: Acinetobacter baumannii
US-09-328-352-943

Query Match 57.1%; Score 12; DB 4; Length 1362;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GTTCGAGATGAT 21
|||||
DB 949 GTTCGAGATGAT 960

RESULT 57
US-09-252-991A-64

Sequence 64, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 64
LENGTH: 1368
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-64

Query Match 57.1%; Score 12; DB 4; Length 1368;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGAAGTTGAG 16
|||||
DB 928 CGAAGTTGAG 939

RESULT 58
US-09-252-991A-6308/c
Sequence 6308, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6308
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6308
```

```
Query Match          57.1%; Score 12; DB 4; Length 1443;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      10 GTTCGAGATGAT 21
      |||||
Db      994 GTTCGAGATGAT 983
```

```
RESULT 59
US-09-351-224E-7/c
; Sequence 7, Application US/09351224E
; Patent No. 6388171
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jon
; APPLICANT: Maddox, Joyce
; APPLICANT: Gilliam, Jacob
; APPLICANT: Folkerts, Otto
; APPLICANT: Crasta, Oswald R.
; TITLE OF INVENTION: Compositions and Methods for Fumonisin
; TITLE OF INVENTION: Detoxification
; FILE REFERENCE: 5718-111
; CURRENT APPLICATION NUMBER: US/09/351,224E
; CURRENT FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: permealase, fully spliced cDNA
US-09-351-224E-7
```

```
Query Match          57.1%; Score 12; DB 4; Length 1578;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 CGTTCGAGATGA 20
      |||||
Db      1109 CGTTCGAGATGA 1098
```

```
RESULT 60
US-09-677-488A-7/c
; Sequence 7, Application US/09677488A
; Patent No. 6482621
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jon
; APPLICANT: Maddox, Joyce
; APPLICANT: Gilliam, Jacob
; APPLICANT: Folkerts, Otto
; APPLICANT: Crasta, Oswald R.
; TITLE OF INVENTION: Compositions and Methods for Fumonisin
; TITLE OF INVENTION: Detoxification
```

```
; FILE REFERENCE: 35718/204100
; CURRENT APPLICATION NUMBER: US/09/677,488A
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/351,224
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: permealase, fully spliced cDNA
US-09-677-488A-7
```

```
Query Match          57.1%; Score 12; DB 4; Length 1578;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 CGTTCGAGATGA 20
      |||||
Db      1109 CGTTCGAGATGA 1098
```

```
RESULT 61
US-09-677-682B-7/c
; Sequence 7, Application US/09677682B
; Patent No. 6534291
; GENERAL INFORMATION:
; APPLICANT: Duvick, Jon
; APPLICANT: Maddox, Joyce
; APPLICANT: Gilliam, Jacob
; APPLICANT: Folkerts, Otto
; APPLICANT: Crasta, Oswald R.
; TITLE OF INVENTION: Compositions and Methods for Fumonisin
; TITLE OF INVENTION: Detoxification
; FILE REFERENCE: 35718/204101
; CURRENT APPLICATION NUMBER: US/09/677,682B
; CURRENT FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/351,224
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1578
; TYPE: DNA
; ORGANISM: Exophiala spinifera
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: permealase, fully spliced cDNA
US-09-677-682B-7
```

```
Query Match          57.1%; Score 12; DB 4; Length 1578;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 CGTTCGAGATGA 20
      |||||
Db      1109 CGTTCGAGATGA 1098
```

```
RESULT 62
US-09-252-991A-354E/c
; Sequence 3548, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
```

```
/ CURRENT APPLICATION NUMBER: US/09/252,991A
/ CURRENT FILING DATE: 1999-02-18
/ PRIOR APPLICATION NUMBER: US 60/074,788
/ PRIOR FILING DATE: 1998-02-18
/ PRIOR APPLICATION NUMBER: US 60/094,190
/ PRIOR FILING DATE: 1998-07-27
/ NUMBER OF SEQ ID NOS: 33142
/ SEQ ID NO 3548
/ LENGTH: 1644
/ TYPE: DNA
/ ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3548
```

```
Query Match          57.1%; Score 12; DB 4; Length 1644;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy          9 CGTTCGAGATGA 20
            |||||
Db          380 CGTTCGAGATGA 369
```

```
RESULT 63
US-09-351-224E-6/c
/ Sequence 6, Application US/09351224E
/ Patent No. 6388171
/ GENERAL INFORMATION:
/ APPLICANT: Duviok, Jon
/ APPLICANT: Maddox, Joyce
/ APPLICANT: Gilliam, Jacob
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Crasta, Oswald R.
/ TITLE OF INVENTION: Compositions and Methods for Fumonisin
/ FILE REFERENCE: 5718-111
/ CURRENT APPLICATION NUMBER: US/09/351,224E
/ CURRENT FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 1764
/ TYPE: DNA
/ ORGANISM: Exophiala spinifera
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: permealase, partially spliced cDNA
US-09-351-224E-6
```

```
Query Match          57.1%; Score 12; DB 4; Length 1764;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy          9 CGTTCGAGATGA 20
            |||||
Db          1113 CGTTCGAGATGA 1102
```

```
RESULT 64
US-09-677-488A-6/c
/ Sequence 6, Application US/09677488A
/ Patent No. 6482621
/ GENERAL INFORMATION:
/ APPLICANT: Duviok, Jon
/ APPLICANT: Maddox, Joyce
/ APPLICANT: Gilliam, Jacob
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Crasta, Oswald R.
/ TITLE OF INVENTION: Compositions and Methods for Fumonisin
/ FILE REFERENCE: 35718/204100
/ CURRENT APPLICATION NUMBER: US/09/677,488A
/ CURRENT FILING DATE: 2000-10-02
```

```
/ PRIOR APPLICATION NUMBER: 09/351,224
/ PRIOR FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 1764
/ TYPE: DNA
/ ORGANISM: Exophiala spinifera
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: permealase, partially spliced cDNA
US-09-677-488A-6
```

```
Query Match          57.1%; Score 12; DB 4; Length 1764;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy          9 CGTTCGAGATGA 20
            |||||
Db          1113 CGTTCGAGATGA 1102
```

```
RESULT 65
US-09-677-682B-6/c
/ Sequence 6, Application US/09677682B
/ Patent No. 6534291
/ GENERAL INFORMATION:
/ APPLICANT: Duviok, Jon
/ APPLICANT: Maddox, Joyce
/ APPLICANT: Gilliam, Jacob
/ APPLICANT: Folkerts, Otto
/ APPLICANT: Crasta, Oswald R.
/ TITLE OF INVENTION: Compositions and Methods for Fumonisin
/ FILE REFERENCE: 35718/204101
/ CURRENT APPLICATION NUMBER: US/09/677,682B
/ CURRENT FILING DATE: 2000-10-02
/ PRIOR APPLICATION NUMBER: 09/351,224
/ PRIOR FILING DATE: 1999-07-12
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 1764
/ TYPE: DNA
/ ORGANISM: Exophiala spinifera
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (0)...(0)
/ OTHER INFORMATION: permealase, partially spliced cDNA
US-09-677-682B-6
```

```
Query Match          57.1%; Score 12; DB 4; Length 1764;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy          9 CGTTCGAGATGA 20
            |||||
Db          1113 CGTTCGAGATGA 1102
```

```
RESULT 66
US-07-754-918A-1
/ Sequence 1, Application US/07754918A
/ Patent No. 5286484
/ GENERAL INFORMATION:
/ APPLICANT: Rodriguez, R.S. et al
/ TITLE OF INVENTION: NICKOTIC SMOKE SMOKE CODING FOR AN
/ TITLE OF INVENTION: OUTER MEMBRANE PROTEIN FROM NEISSERIA MENINGITIDIS AND USE
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: Stanger, Michaelson, Spivak and Wallace, Bq.
```

STREET: Parkway 109 Office Center, 328 Newman Springs
STREET: Road, P. O. Box 8489
CITY: Red Bank
STATE: New Jersey
COUNTRY: USA
ZIP: 07701

COMPUTER READABLE FORM:

MEDIUM TYPE: 5 1/4" 360KB IBM compatible diskette
COMPUTER: IBM PS/2 Model 80
OPERATING SYSTEM: MS-DOS 5.0
SOFTWARE: Microsoft Word 5.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/754,918A
FILING DATE: 19910905
CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Michaelson, Peter L.
REGISTRATION NUMBER: 30090
REFERENCE/DOCKET NUMBER: Centro-2R
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 530-6671
TELEFAX: (908) 530-6584
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:

LENGTH: 1836 bp
TYPE: NUCLEOTIDE WITH CORRESPONDING AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: genomic DNA

ORIGINAL SOURCE:

ORGANISM: N. meningitidis group B

IMMEDIATE SOURCE: Strain B:4:P1:15 isolated in Cuba

FEATURE: From 1 to 1830 bp mature protein

OTHER INFORMATION:

PROPERTIES: Gene coding for P64k protein from outer membrane
OTHER INFORMATION: of N. meningitidis

US-07-754-918A-1

Query Match

Best Local Similarity 57.1%; Score 12; DB 1; Length 1836;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGACGTT 12
|||||

Db 449 TCGTCGACGTT 460

RESULT 67

US-09-555-000-1
Sequence 1, Application US/09555000
Patent No. 6489108

GENERAL INFORMATION:

APPLICANT: Genencor International, Inc.

TITLE OF INVENTION: Proteases from Gram Positive Organisms

FILE REFERENCE: GC390-PCT

CURRENT APPLICATION NUMBER: US/09/555,000

CURRENT FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: PCT/US98/26971

PRIOR FILING DATE: 1998-12-17

NUMBER OF SEQ ID NOS: 2

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 1900

TYPE: DNA

ORGANISM: Bacillus subtilis

FEATURE:

NAME/KEY: CDS

LOCATION: (134)...(1774)

US-09-555-000-1

Query Match

Best Local Similarity 57.1%; Score 12; DB 4; Length 1900;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GTCGACGTTG 14
|||||

Db 1108 GTCGACGTTG 1119

RESULT 68

US-08-358-117-1/c
Sequence 1, Application US/08358117
Patent No. 5608147

GENERAL INFORMATION:

APPLICANT: Kaphammer, Bryan J.

TITLE OF INVENTION: tlda Gene Selectable Markers in Plants and the

TITLE OF INVENTION: Use Thereof

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Steine, Kessler, Goldstein & Fox

STREET: 1100 New York Avenue, Suite 600

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/358,117

FILING DATE: 15-DEC-1994

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1405.0030001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2600

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2058 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 751...1611

US-08-358-117-1

Query Match

Best Local Similarity 57.1%; Score 12; DB 1; Length 2058;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACCTTCGAGTG 19
|||||

Db 1016 ACCTTCGAGTG 1005

RESULT 69

US-08-470-588-1/c
Sequence 1, Application US/08470588
Patent No. 6100446

GENERAL INFORMATION:

APPLICANT: STREBER, WOLFGANG R.

APPLICANT: TIMMIS, KENNETH N.

APPLICANT: ZENK, WERNHART H.

TITLE OF INVENTION: MICROORGANISMS AND PLASMIDS FOR

TITLE OF INVENTION: 2,4-DICHLOROPHENOXACETIC ACID (2,4-D) MONOOXYGENASE

TITLE OF INVENTION: FORMATION AND PROCESS FOR THE PRODUCTION OF THESE PLASMIDS

TITLE OF INVENTION: AND STRAINS

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: FROMMER LAWRENCE & HAUG LLP

STREET: 745 FIFTH AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10151
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470.588
FILING DATE: 07-JUN-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: LAWRENCE, WILLIAM F.
REGISTRATION NUMBER: 28,029
REFERENCE/DOCKET NUMBER: 514413-3526
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-588-0800
TELEFAX: 212-588-0500
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2058 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-470-588-1

Query Match 57.1%; Score 12; DB 3; Length 2058;
Best Local Similarity 100.0%; Pred. No. 97;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 ACGTTCGAGATG 19
|||||
Db 1016 ACGTTCGAGATG 1005

RESULT 70
US-08-528-026C-3/C
Sequence 3, Application US/08528026C
Patent No. 6248566
GENERAL INFORMATION:
APPLICANT: IMANAKA, Tadayuki
APPLICANT: TERADA, Yoshihobu
APPLICANT: TAKAHARA, Takeshi
APPLICANT: YANASE, Michiyo
APPLICANT: OKADA, Shigetaka
APPLICANT: TAKATA, Hiroki
APPLICANT: NAKAMURA, Hiroyasu
APPLICANT: FUJII, Kazutoshi
TITLE OF INVENTION: GLUCAN HAVING CYCLIC STRUCTURE AND METHOD FOR PRODUCING THE SAME
FILE REFERENCE: 9900-0002.20
CURRENT APPLICATION NUMBER: US/08/528,026C
CURRENT FILING DATE: 1995-09-13
PRIOR APPLICATION NUMBER: US 08/445,152
PRIOR FILING DATE: 1995-03-31
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Version 3.0
SEQ ID NO: 3
LENGTH: 2426
TYPE: DNA
ORGANISM: Bacillus stearothermophilus (Strain TB814)
FEATURE:
NAME/KEY: misc feature
LOCATION: (385) (392)
OTHER INFORMATION: S SD sequence
NAME/KEY: misc_feature
LOCATION: (402) (2357)
OTHER INFORMATION: P CDS
US-08-528-026C-3

Query Match 57.1%; Score 12; DB 3; Length 2426;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CGTTCGAGATGA 20
|||||
Db 1278 CGTTCGAGATGA 1267

RESULT 71
US-09-221-017B-225
Sequence 225, Application US/09221017B
Patent No. 6444799
GENERAL INFORMATION:
APPLICANT: ROSE, Bruce C.
TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
NUMBER OF SEQUENCES: 1120
CORRESPONDENCE ADDRESS:
ADDRESSER: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FastSeq for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,017B
FILING DATE: 23-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1182
FILING DATE: 31-DEC-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP1546
FILING DATE: 30-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PP2911
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Monroy, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 225:
SEQUENCE CHARACTERISTICS:
LENGTH: 2572 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...2572
US-09-221-017B-225

Query Match 57.1%; Score 12; DB 4; Length 2572;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GGTTCGAGATGAT 21
|||||
Db 936 GTTCGAGATGAT 947

RESULT 72

US-09-619-353-13
; Sequence 13, Application US/09619353
; Patent No. 6410249
; GENERAL INFORMATION:
; APPLICANT: Ngai, John
; APPLICANT: Speca, David J.
; APPLICANT: Lin, David M.
; APPLICANT: Isacoff, Erud Y.
; APPLICANT: Diltman, Andrew H.
; APPLICANT: Fan, Jinhong
; TITLE OF INVENTION: Odorant Receptors
; FILE REFERENCE: B99-038-2
; CURRENT APPLICATION NUMBER: US/09/619,353
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/144,766
; PRIOR FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 2595
; TYPE: DNA
; ORGANISM: Brachydanio rerio (zebrafish)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(2592)
US-09-619-353-13

Query Match 57.1%; Score 12; DB 4; Length 2595;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20
|||||
Db 1964 CGTTCGAGATGA 1975

RESULT 73

US-09-221-017B-462/C
; Sequence 462, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: PP2811
FILING DATE: 09-APR-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU98/01023
FILING DATE: 10-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: MONROY, Gladys H
REGISTRATION NUMBER: 32,430
REFERENCE/DOCKET NUMBER: 27340-20021.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-813-5600
TELEFAX: 650-494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 462:
SEQUENCE CHARACTERISTICS:
LENGTH: 2760 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: UNKNOWN
ORIGINAL SOURCE:
ORGANISM: PORPHYROMONAS GINGIVALIS
FEATURE:
NAME/KEY: misc feature
LOCATION: 1...2760
US-09-221-017B-462

Query Match 57.1%; Score 12; DB 4; Length 2760;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 ACGTTCGAGATG 19
|||||
Db 2236 ACGTTCGAGATG 2285

RESULT 74

US-09-252-991A-3523
; Sequence 3523, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 3523
; LENGTH: 2832
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-3523

Query Match 57.1%; Score 12; DB 4; Length 2832;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 CGTTCGAGATGA 20
|||||
Db 1490 CGTTCGAGATGA 1501

RESULT 75

US-08-936-165A-66/C
; Sequence 66, Application US/08936165A
; Patent No. 6348582

```

/ GENERAL INFORMATION:
/ APPLICANT: Black, Michael
/ APPLICANT: Burnham, Martin
/ APPLICANT: Hodgson, John
/ APPLICANT: Knowles, David
/ APPLICANT: Lonetto, Michael
/ APPLICANT: Nicholas, Richard
/ APPLICANT: Pratt, Julie
/ APPLICANT: Reichard, Richard
/ APPLICANT: Rosenberg, Martin
/ APPLICANT: Ward, Judith
/ TITLE OF INVENTION: No. 6348582e1 Prokaryotic Polynucleotides,
/ TITLE OF INVENTION: Polypeptides and Their Uses
/ NUMBER OF SEQUENCES: 534
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: SmithKline Beecham Corporation
/ STREET: 709 Swedeland Road
/ CITY: King of Prussia
/ STATE: PA
/ COUNTRY: USA
/ ZIP: 19406-0939
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/936,165A
/ FILING DATE: 24-SEP-1997
/ CLASSIFICATION: 536
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/027,032
/ FILING DATE: 24-SEP-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gimm1, Edward R
/ REGISTRATION NUMBER: 38, 891
/ REFERENCE/DOCKET NUMBER: P50549
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 610-270-4478
/ TELEFAX: 610-270-5090
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 66:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2854 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: Genomic DNA
/ US-08-936-165A-66

Query Match      57.1%; Score 12; DB 4; Length 2854;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      9 CGTCGAGATGA 20
        |||||
Db      1984 CGTCGAGATGA 1973

```

Search completed: December 17, 2003, 10:01:51
 Job time : 67 secs

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